



well-known in the art. The transgenic non-human animal can be from any species, including avians and non-human mammals. According to this aspect of the invention, suitable non-human mammals include mice, rats, rabbits, guinea pigs, goats, sheep, pigs and cattle. Suitable avians include chickens, ducks, geese, quail, turkeys and pheasants.

The nucleic acid encoding the CATERPILLER polypeptide or functional fragment can be stably incorporated into cells within the transgenic animal (typically, by stable integration into the genome or by stably maintained episomal constructs). It is not necessary that every cell contain the transgene, and the animal can be a chimera of modified and unmodified cells, as long as a sufficient number of cells comprise and express the nucleic acid encoding the CATERPILLER polypeptide or functional fragment so that the animal is a useful screening tool.

Exemplary methods of using the transgenic non-human animals of the invention for *in vivo* screening of compounds that modulate inflammatory response (both pro- and anti-inflammatory responses), cell survival (both pro- and anti-survival) and/or the activity of a CATERPILLER polypeptide comprise administering a test compound to a transgenic non-human animal (e.g., a mammal such as a mouse) comprising an isolated nucleic acid encoding a CATERPILLER polypeptide or functional fragment thereof stably incorporated into the genome, administering a test compound to the transgenic non-human animal, and detecting whether the test compound modulates inflammatory response, cell survival and/or CATERPILLER polypeptide activity (or the activity of a functional fragment). Other illustrative methods of the invention can be carried out to identify compounds that modulate MHC-II pathway activity, Toll-like receptor pathway activity, or NF- κ B activity *in vivo*.

It is known in the art how to measure these responses *in vivo*. Illustrative approaches include observation of changes that can be studied by gross examination (edema, redness, swelling, fever, tenderness), histopathology (cellular infiltrates, cell activation markers, phagocytosis, dead cells), changes in cytokine profiles, and cell surface markers (e.g., changes in TNF α , myeloperoxidase or CD69).

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Limits Preview/Index History Clipboard Details

Display **GenBank** Show **5** Send to

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

1: [AF389420](#). Reports *Homo sapiens* NOD2...[gi:28866920] [Links](#)

LOCUS AF389420 5601 bp mRNA linear PRI 06-MAR-2003

DEFINITION Homo sapiens NOD27 (NOD27) mRNA, complete cds.

ACCESSION AF389420

VERSION AF389420.1 GI:28866920

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 5601)

AUTHORS Dowds, T.A., Masumoto, J., Chen, F.F., Ogura, Y., Inohara, N. and Nunez, G.

TITLE Regulation of cryopyrin/Pypaf1 signaling by pyrin, the familial Mediterranean fever gene product

JOURNAL Biochem. Biophys. Res. Commun. 302 (3), 575-580 (2003)

PUBMED 12615073

REFERENCE 2 (bases 1 to 5601)

AUTHORS Inohara, N.

TITLE Direct Submission

JOURNAL Submitted (04-JUN-2001) CCGC, University of Michigan, 1500 E.

Medical Center Dr., Ann Arbor, MI 48109, USA

FEATURES	Location/Qualifiers
----------	---------------------

```
source      1..5601
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /chromosome="16"
```

```

gene      1..5601
          /gene="NOD27"
CDS       1..5601
          /gene="NOD27"
          /note="NOD family member"
          /codon_start=1

```

```

/product="NOD27"
/protein_id="AA059377.1"
/db xref="GI:28866921"

```

```
/translation="MDPVGLQLGNKNLWSCLVRLLTQDPEWLNAMKFFLPNTDLSR
NETLDPEQVRVILQLNKLHVQGSQDQWQSFQHCVMQLEVPDLEVLLSTFGYDDGFTS
QLGAEGKSQPESQLHHGLKRPHQSCGSSPRRKQCKKQQLLAKKYLLQLRTSAQQRYR
SQIPGSGQPFAFHQVYVPPILRRATASLDTPEGAIMGDVKVEDGADVSIQDLFNTRVN
KGPRVTVLLGKAGMGKTTLAHRLCQKWAEGHLNCFQALFLFEFRQLNLITRFLTPSEL
LFDLYLSPESDHDQTVFYQYLEKNADQVLLIFDGLDEALQPMGPDGPGPVLTFLSHLCNG
TLLPGCRVMATSRPGKLPACLPAEAAMVHMLGFDGPRVEEYVNHFFSAQPSREGALVE
LQTNGRLRSLCAVPALCQVACLCLHLLLPDHAPGQSVALLPNMTOLYMOMVLALSPPG
```


HLPTSSLLDLGEVALRGLETGKVI FYAKDIAPPLIAFGATHSLLTSFCVCTGPGHQQT
 GYAFTHLSLQEFALAHLMASPKVNKDTLTQYVTLHSRWVQRTKARLGLSDHLPFTFLA
 GLASCTCRPFLSHLAQGNEDCVGAKQAAVVQVLKKLATRKLTPGVVVELCHCVDETQE
 PELASLTAQSLPYQLPFHNFPLTCTDLATLTNILEHREAPIHLDGFCPLPHCPAL
 VGCGQIENLSFKSRKCGDAFAEALSRLPTMGRLQMLGLAGSKITARGISHLVKALPL
 CPQLKEVSFRDNQSLDQVVLNIVEVLPHLPRLRKLDLSSNSICVSTLLCLARVAVTCF
 TVRMLQARERTIIIFLLSPPTETTAELQRAPDLQESDQQRKGAQSRSLTLRLQKQQLQV
 HDAEALIALLOEGPHLEEVLDLGNQLEDEGCRLMAEAAASQLHIARKLDSLNDGLSVAG
 VHCVLRAVSACWTLAELHISLQHKTVIFMFAQEPEEQKGPQERAAFLDSLMLQMPSEL
 PLSSRRMRLTHCGLQEKHLEQLCKALGGSCHLGLHLHLDGSGNALGDEGAARLAQLLP
 LGALQSLNLSENGLSLDAVLGLVRCFSTLQWLFRDLISFESQHILLRGDKTSRDMWAT
 GSLPDFPAAAKFLGFRQRCIPRSLCLSECPLEPPSLTRLCLATLKDCPGPLELQLSCEF
 LSDQSLETLDDCLPQLPQLSLLQLSQTGLSPKSPFLLANTLSLCPRVKKVDLRLSLHHA
 TLHFRSNEEEEGVCCGRFTGCSLSQEHVESLCWLLSKCKDLSDQVLDLSANLLGDSGLRC
 LLECLPQVPISGLLDLSHNSISQESALYLLETLPSCPRVREASVNLGSEQSFIHFSR
 EDQAGKTLRLSECSFRPEHVSRLATGLSKSLQLTELTLTQCCLGQKQLAILLSLVGRP
 AGLFSLRVQEPWADRARVLSLLEVCAQASGSVTEISISSETQQQLCVQLEFPQREENPE
 AVALRLAHCDLGAHSLLVGQLMETCARLQQLSLSQVNLCEDDDASSLLQLSLLLSLS
 ELKTFRLTSSCVSTEGLAHLASGLGHCHHLEELDLSNNQFDEEGTKALMRALEGKMWL
 KRLDLSHLLNSSTLALLTHRLSQMTCLQSLRLNRNSIGDVGCCHLSEALRAATSLEE
 LDLSHNQIGDAGVQHLATILPGLPELRKIDLSGNSISSAGGVQLAESLVLCCRLEELM
 LGCNALGDPTALGLAQELPQHLRVLHLPFSLHLPGLGPGGALSQAALDGSPLHEEISLAEN
 NLAGGVLRFCMELPLLRQIDLVSCKIDNQTAKLTTSSFTSCPALEVILLSWNLLGDEA
 AAELAQVLPKMGRCLKRVDLEKNQITALGAWLLAEGLAQSSIIQVIRLWNNPIPCDMAQ
 HLKSQEPRLDFAFFDNQPAPWGT"

ORIGIN

1	atggacccccg	ttggcctcca	gctcggcaac	aagaacctgt	ggagctgtct	tgtgaggctg
61	ctcaccaaaag	accagaatg	gctgaacgcc	aagatgaagt	tcttcctccc	caacacggac
121	ctggattcca	ggaacgagac	cttggaccct	gaacagagag	tcattcctgca	actcaacaag
181	ctgcatgtcc	aggggttcgga	cacctggcag	tctttcattc	attgcgtgtg	catgcagctg
241	gaggtgcctc	tggacctgga	ggtgcttctg	ctaagtactt	tgggctatga	tgatgggttc
301	accagccagc	tgggagctga	ggggaaaagc	caacctgaat	ctcagctcca	ccatggcctg
361	aagcgcccac	atcagagctg	tgggtcctca	ccccgccgga	agcagtgcaa	gaagcagcag
421	ctagagttgg	ccaagaagta	cctgcagctc	ctgcggacct	ctgcccagca	gcgctacagg
481	agccaaaatcc	ctgggtcagg	gcagccccac	gccttcacc	aggtctatgt	ccctccaatc
541	ctgcgccggg	ccacagcatc	cttagacact	ccggaggggg	ccattatggg	ggacgtcaag
601	gtggaagatg	gtgctgacgt	gagcatctcg	gacctcttca	acaccagggt	taacaagggc
661	ccgaggggtga	ccgtgctttt	ggggaaggct	ggcatgggca	agaccacgct	ggcccaccgg
721	ctctgccaga	agtgggcaga	gggccatctg	aactgtttcc	aggccctgtt	cccttttgaa
781	ttccgccagc	tcaacttgat	cacgaggttc	ctgacaccgt	ccgagctcct	ttttgatctg
841	tacctgagcc	ctgaatcgga	ccacgacact	gtcttccagt	acctggagaa	gaacgctgac
901	caagtccctgc	tgatctttga	tgggctagat	gaggccctcc	agcctatggg	tctgatggc
961	ccaggccag	tcctcaccct	tttctcccat	ctctgcaatg	ggaccctcct	gcctggctgc
1021	cgggtgatgg	ctacctccc	tccagggaag	ctgcctgcct	gcctgcctgc	agaggcagcc
1081	atggtccaca	tggtgggctt	tgatgggcca	cgggtggaag	aatatgtgaa	tcacttcttc
1141	agcgcgccagc	catcgccgga	gggggccctg	gtggagttac	agacaaatgg	acgtctccga
1201	agcctgtgtg	cgggtgccgc	actgtgccaa	gtgcctgtc	tctgcctcca	ccatctgctt
1261	cctgaccacg	ccccaggcca	gtctgtggcc	ctcctgcccc	acatgactca	gctctatatg
1321	cagatggtgc	tcgccctcag	ccccctggg	cacttgcccc	cctcgtccct	actggacctg
1381	ggggagggtg	ccctgagggg	cctggagaca	gggaagggtta	tcttctatgc	aaaagatatt
1441	gtccaccct	tgatagcttt	tggggccact	cacagcctgc	tgacttcctt	ctgcgtctgc
1501	acaggccctg	ggcaccagca	gacaggctat	gctttcacc	acctcagcct	gcaggagttt
1561	cttgctgccc	tgcacctgat	ggccagcccc	aaggtgaaca	aagacacact	taccagtat
1621	gttaccctcc	attcccgtg	ggtacagcgg	accaaagcta	gactgggcct	ctcagaccac
1681	ctccccacct	tcctggcggg	cctggcatcc	tgcacctgcc	gccccctcct	tagccacctg
1741	gcgcagggca	atgaggactg	tgtgggtgcc	aagcaggctg	ctgtagtga	ggtgttgaag
1801	aagttggcca	cccgaagct	cacagggcca	aaggtttag	agctgtgtca	ctgtgtggat
1861	gagacacagg	agcctgagct	ggcagctc	accgcacaaa	gcctccccta	tcaactgccc
1921	ttccacaatt	tccactgac	ctgcaccgac	ctggccaccc	tgaccaacat	cctagagcac
1981	agggaggccc	ccatccacct	ggattttgat	ggctgtcccc	tggagcccca	ctgcctgag

```
2041 gctctggtag gctgtgggca gatagagaat ctcagcttta agagcaggaa gtgtggggat
2101 gcctttgcag aagccctctc caggagcttg ccgacaatgg ggaggctgca gatgctgggg
2161 ttagcaggaa gtaaaatcac tgcccagggc atcagccacc tggtgaaagc tttgcctctc
2221 tgtccacagc tgaaagaagt cagttttcgg gacaaccagc tcagtgacca ggtggtgctg
2281 aacattgtgg aggttctccc tcacctacca cggctccgga agcttgacct gagcagcaac
2341 agcatctgcg tgtcaacct actctgcttg gcaagggtgg cagtacagtg tcctaccgtc
2401 aggatgcttc aggccaggga gcggaccatc atcttccttc tttccccgcc cacagagaca
2461 actgcagagc taaaagagc tccagacctg caggaaagtg acggccagag gaaaggggct
2521 cagagcagaa gcttgacgct caggctgcag aagtgtcagc tccaggtcca cgatgcggag
2581 gccctcatag ccctgctcca ggaaggccct cacctggagg aagtggacct ctcagggaac
2641 cagctggaag atgaaggctg tcggctgatg gcagaggctg catcccagct gcacatcgcc
2701 aggaagctgg acctcagcga caacgggctt tctgtggccg ggtgctattg tgtgtgagg
2761 gccgtgagtg cgtgctggac cctggcagag ctgcacatca gcctgcagca caaaactgtg
2821 atcttcatgt ttgcccagga gccagaggag cagaaggggc cccaggagag ggctgcattt
2881 cttgacagcc tcattgctcca gatgccctc gagctgcctc tgagctcccg aaggatgagg
2941 ctgacacatt gtggcctcca agaaaagcac ctagagcagc tctgcaaggc tctgggagga
3001 agctgccacc tcggtcacct ccacctcgac ttctcaggca atgctctggg ggatgaagggt
3061 gcagcccggc tggtcagct gctcccaggg ctgggagctc tgcagtcctt gaacctcagt
3121 gagaacggtt tgtccctgga tgccgtgttg ggcttggttc ggtgcttctc cactctgcag
3181 tggctcttcc gcttggacat cagctttgaa agccaacaca tcctcctgag aggggacaag
3241 acaagcaggg atatgtgggc cactggatct ttgccagact tcccagctgc agccaagttc
3301 ttagggttcc gtcagcgtg catccccagg agcctctgcc tcagtgaagt tcctctggag
3361 cccccaagcc tcaccgcct ctgtgccact ctgaaggact gcccgggacc cctggaactg
3421 caattgtcct gtgagttcct gagtgaccag agcctggaga ctctactgga ctgcttacct
3481 caactccctc agctgagcct gctgcagctg agccagacgg gactgtcccc gaaaagcccc
3541 ttcttctgct ccaacacctt aagcctgtgt ccacgggtta aaaagggtga tctcaggtcc
3601 ctgcaccatg caactttgca cttcagatcc aacgaggagg aggaaggcgt gtgctgtggc
3661 aggttcacag gctgcagcct cagccaggag cacgtagagt cactctgctg gttgctgagc
3721 aagtgtaaag acctcagcca ggtggatctc tcagcaaacc tgctgggcca cagcggactc
3781 agatgccttc tggaatgtct gccgcagggt cccatctccg gtttgcttga tctgagtcac
3841 aacagcattt ctcaggaaaag tgccctgtac ctgctggaga cactgccctc ctgcccacgt
3901 gtccgggagg cctcagtgaa cctgggctct gagcagagct tccggattca cttctccaga
3961 gaggaccagg ctgggaagac actcaggcta agtgagtga gcttccggcc agagcacgtg
4021 tccaggctgg ccaccggctt gagcaagtcc ctgcagctga cggagctcac gctgaccag
4081 tctgtcctgg gccagaagca gctggccatc ctctgagct tgggtggggcg acccgagggt
4141 ctgttcagcc tcagggtgca ggagccgtgg gcggacagag ccagggttct ctccctgtta
4201 gaagtctgct cccaggcctc aggcagtgtc actgaaatca gcatctccga gaccagcag
4261 cagctctgtg tccagctgga atttctctgc caggaaagga atccagaagc tgtggcactc
4321 aggttggtct actgtgacct tggagcccac cacagccttc ttgtcgggca gctgatggag
4381 acatgtgcca ggctgcagca gctcagcttg tctcagggtta acctctgtga ggacgatgat
4441 gccagttccc tgetgctgca gagectctct ctgtccctct ctgagctgaa gacatttcgg
4501 ctgacctcca gctgtgtgag caccgagggt ctcgcccacc tggcatctgg tctgggccac
4561 tgccaccact tggaggagct ggacttgtct aacaatcaat ttgatgagga gggcaccaag
4621 gcgctgatga gggcccttga ggggaaatgg atgctaaaga ggctggacct cagtcacctt
4681 ctgctgaaca gctccacctt ggcttgcctt actcacagac taagccagat gacctgcctg
4741 cagagcctca gactgaacag gaacagtatc ggtgatgtcg gttgctgcca cctttctgag
4801 gctctcaggg ctgccaccag cctagaggag ctggacttga gccacaacca gattggagac
4861 gctggtgtcc agcacttagc taccatcctg cctgggctgc cagagctcag gaagatagac
4921 ctctcaggga atagcatcag ctcagccggg ggagtgcagt tggcagagtc tctcgttctt
4981 tgcaggcgcc tggaggagtt gatgcttggc tgcaatgccc tgggggatcc cacagccctg
5041 gggctggctc aggagctgcc ccagcacctg agggtcctac acctaccatt cagccatctg
5101 ggcccagggt gggccctgag cctggcccag gccctggatg gatcccccca tttggaagag
5161 atcagcttgg cggaaaacaa cctggctgga ggggtcctgc gtttctgtat ggagctcccg
5221 ctgctcagac agatagacct ggtttcctgt aagattgaca accagactgc caagctcctc
5281 acctccagct tcacgagctg ccctgccctg gaagtaatct tgctgtcctg gaatctcctc
5341 ggggatgagg cagctgccga gctggcccag gtgctgccga agatggggcg gctgaagaga
5401 gtggacctgg agaagaatca gatcacagct ttgggggcct ggctcctggc tgaaggactg
5461 gcccaggggt ctagcatcca agtcacccg ccttggaata accccattcc ctgcgacatg
5521 gcccagcacc tgaagagcca ggagcccagg ctggactttg ccttctttga caaccagccc
5581 caggccctt ggggtacttg a
```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42

My NCBI
[Sign In]
[Register]

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Limits Preview/Index History Clipboard Details

Display Show Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒☐ 1: [AF526389](#). Reports Homo sapiens cryo...[gi:24461921][Links](#)

LOCUS AF526389 761 bp DNA linear PRI 14-JAN-2003

DEFINITION Homo sapiens cryopyrin (CIAS1) gene, intron 6.

ACCESSION AF526389

VERSION AF526389.1 GI:24461921

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiensEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 761)

AUTHORS Hoffman,H.M., Mueller,J.L., Broide,D.H., Wanderer,A.A. and
Kolodner,R.D.TITLE Mutation of a new gene encoding a putative pyrin-like protein
causes familial cold autoinflammatory syndrome and Muckle-Wells
syndrome

JOURNAL Nat. Genet. 29 (3), 301-305 (2001)

PUBMED [11687797](#)

REFERENCE 2 (bases 1 to 761)

AUTHORS Hoffman,H.M., Gregory,S.G., Mueller,J.L., Tresieras,M.,
Broide,D.H., Wanderer,A.A. and Kolodner,R.D.TITLE Fine structure mapping of CIAS1: identification of an ancestral
haplotype and a common FCAS mutation, L353P

JOURNAL Hum. Genet. 112 (2), 209-216 (2003)

PUBMED [12522564](#)

REFERENCE 3 (bases 1 to 761)

AUTHORS Hoffman,H.M. and Mueller,J.L.

TITLE Direct Submission

JOURNAL Submitted (02-JUL-2002) Medicine, UCSD, 9500 Gilman Drive, La
Jolla, CA 92093, USA

FEATURES Location/Qualifiers

source

1..761
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
/map="1q44"gene<1..>761
/gene="CIAS1"
/note="cryopyrin"intron1..761
/gene="CIAS1"
/note="similar to the sequence of AC104335"
/number=6

ORIGIN

```
1 gatctatcga ttggggcata atatcccata gtgtgcttta ccataattta tttaatcaaa
61 tcatgcattt tgggataact gttcttttcc actattacaa acaactctgc aaaaagcaca
121 tttgtatata tagttttatg catgtgtatt tgctttgaga taggtatcta taagtggcat
181 taatcagtcg agacttttat gcattttatg tgtaggtac agccatacat gtggctgtgt
241 gttagggtata gcctatgggt taggcatagc ctgtgtgtta ggtatagcct atgggttagg
301 tatagcctac gtgttaggta tagcctatgt gttagggtata gcctatgtgt taggtatagc
361 tacatttttt tctctcgaac tttgggtcct catctctggc tgcatttgt gtactgcctg
421 tctcaatact gctcaagggt cacacatgct gagcatttgc aacattgggt taattatcat
481 accccacctt ccacccccgt tctctgacct gctcctgccc tcttcctcct gcctcattga
541 atagtggggc tttccaggag gctgctgagt gagtaaacgg gggacgggtcc taaatgctct
601 gctttcgggt ccctctacca ctcatcacta caccagaggg aactttttta gatgcaaatt
661 tgaaaatatt gaccctttgt tcaaaaatct tcaaaagtgc ttctctgcag tcagagtgc
721 atcttagctt ggcacacaag ctgtccctga tactgcctc t
```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42




[My NCBI](#)
[Sign In](#)
[Register](#)

[PubMed](#) [Nucleotide](#) [Protein](#) [Genome](#) [Structure](#) [PMC](#) [Taxonomy](#) [OMIM](#) [Books](#)
 Search for

[Limits](#) [Preview/Index](#) [History](#) [Clipboard](#) [Details](#)

Display ☒ Show ☒ Send to ☒

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [AK025131](#). Reports Homo sapiens cDNA...[gi:10437587]

[Links](#)

LOCUS AK025131 2404 bp mRNA linear PRI 13-SEP-2003
DEFINITION Homo sapiens cDNA: FLJ21478 fis, clone COL05012.
ACCESSION AK025131
VERSION AK025131.1 GI:10437587
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
REFERENCE 1
AUTHORS Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
 Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
 Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2404)
AUTHORS Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
 Shibahara,T., Tanaka,T. and Nakamura,Y.
TITLE Direct Submission
JOURNAL Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
 University of Tokyo, Laboratory of Genome Structure Analysis, Human
 Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
 Japan (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
 Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
 International Trade and Industry of Japan; cDNA full insert
 sequencing: Research Association for Biotechnology; cDNA library
 construction, 5'- & 3'-end one pass sequencing: Department of
 Virology and Human Genome Center, Institute of Medical Science,
 University of Tokyo (partly supported by Science and Technology
 Agency).
FEATURES
 source Location/Qualifiers
 1..2404
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="COL05012"
 /tissue_type="colon"
 /clone_lib="COL"
 /note="cloning vector pME18SFL3"
 CDS 148..1812
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="BAB15075.1"

```
/db_xref="GI:10437588"  
/translation="MAYAARTMGKLAYEGVSSRKTYFSEEDVCGCLEAGIRTEEEFQL  
LHIFRRDALRFFLAPCVEPGRAGTFVFTVPAMQEYLAALYIVLGLRKTTTLQKVGKEVA  
ELVGRVGEDVSLVLGIMAKLLPLRALPLLFNLIKVVPRVFGRMVGKSREAVAQAMVLE  
MFREEDYYNDDVLDQMGASILGVEGPRRHPDEPPEDEVFELFPMFMGGLLSAHNRAVL  
AQLGCPPIKNLDALENAQAIKKLGLGRQVLPPELDDLHFFHYEFQNRFSAEVLSS  
LRQLNLGVRMTPVKCTVVAVLGSGRHALDEVNLASCQLDPAGLRTLLPVFLRARKL  
GLQLNSLGPEACKDLRDLRLDQCCQITTLRLSNNPLTEAGVAVLMEGLAGNTSVTHLS  
LLHTGLGDEGLELLAAQLDRNRQLQELNVAYNGAGDTAALALARAAREHPSLELLHLY  
FNELSSSEGRQVLRDLGGAEEGARVVVSLTEGTAVSEYWSVILSEVQRNLNSWDRARV  
QRHLELLLRDLEDSESRGATLNPWRKAQLLRVEGEVRALLEQLGSSGS"
```

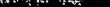
ORIGIN

```
1  tattgctggc  tcgtttgtgc  caccttgcac  ttcctgcatg  cccccacgcc  tgctgggagc  
61  acccttataa  gcatctatac  cagcttcctg  cgcctcaact  tcagcgggga  aaccctggac  
121 agcactgacc  cctccaattt  gtccctgatg  gcctatgcag  cccgaacct  gggcaagtgc  
181 gcctatgagg  ggggtgtctc  cgcgaagacc  tacttctctg  aagaggatgt  ctgtggctgc  
241 ctggaggctg  gcatcaggac  ggaggaggag  tttcagctgc  tgcacatctt  ccgtcgggat  
301 gccctgaggt  ttttcctggc  cccatgtgtg  gagccagggc  gtgcaggcac  cttcgtgttc  
361 accgtgccc  ccatgcagga  atacctggct  gccctctaca  ttgtgctggg  tttgcgcaag  
421 acgacctgc  aaaagggtgg  caaggaagtg  gctgagctcg  tgggcccgtg  tggggaggac  
481 gtcagcctg  tactgggcat  catggccaag  ctgctgcctc  tgcgggctct  gcctctgctc  
541 ttcaacctga  tcaagggtgt  tccacgagtg  tttgggcgca  tgggtgggta  aagccgggag  
601 gcggtggctc  aggccatggt  gctggagatg  tttcgagagg  aggactacta  caacgatgat  
661 gttctggacc  agatgggcgc  cagtatcctg  ggcgtggagg  gccccggcg  ccaccagat  
721 gagccccctg  aggatgaagt  cttcgagctc  ttcccatgt  tcatggggg  gcttctctct  
781 gccacaacc  gagctgtgct  agctcagctt  ggctgcccc  tcaagaacct  ggatgccctg  
841 gagaatgcc  aggccatcaa  gaagaagctg  ggcaagctgg  gccggcaggt  gctgccccca  
901 tcagagctcc  ttgaccacct  cttcttcac  tatgagttcc  agaaccagcg  cttctccgct  
961 gaggtgctca  gctccctgcg  tcagctcaac  ctggcaggtg  tgcgcatgac  accagtcaag  
1021 tgcacagtgg  tggcagctgt  gctgggcagc  ggaaggcatg  ccctggatga  ggtgaacttg  
1081 gcctcctgcc  agctagatcc  tgctgggctg  cgcacactcc  tgctgtctt  cctgctgccc  
1141 cggaagctgg  gcttgcaact  caacagcctg  ggccctgagg  cctgcaagga  cctccgagac  
1201 ctggtgctgc  atgaccagtg  ccaaattacc  aactgcggc  tgtccaacaa  cccgctgacg  
1261 gaggcaggtg  ttgcccgtgt  aatggagggg  ctggcaggaa  acacctcagt  gacgcacctg  
1321 tccctgctgc  acacgggcct  tggggacgaa  ggctggagc  tgctggctgc  ccagctggac  
1381 cgcaaccggc  agctgcagga  gctgaacgtg  gcgtacaacg  gtgctggtga  cacagcggcc  
1441 ctggccctgg  ccagagctgc  ccgggagcac  ccttcctgg  aactgctaca  cctctacttc  
1501 aatgagctga  gctcagaggg  ccgccaggtc  ttgcgagact  tggggggtgc  tgctgaaggt  
1561 ggtgcccggg  tgggtggtgt  actgacagag  gggacggcgg  tgtcagaata  ctggtcagtg  
1621 atcctcagtg  aagtccagcg  gaacctcaat  agctgggatc  gggcccgggt  tcagcgacac  
1681 cttgagctcc  tactgcggga  tctggaagat  agccgggggt  ccaccttaa  tccttgccgc  
1741 aaggcccagc  tgctgcgagt  ggagggcgag  gtcagggcc  tcctggagca  gctgggaagc  
1801 tctggaagct  gagacactgg  cggcaggcac  ctagctatgt  gacctggc  cctaaacctt  
1861 ttccctctgt  ggccctctgg  cttgcactgc  tccctctaga  aagattcctt  caggtctgga  
1921 ggcagaggaa  tgggcatagc  tgagccagtt  gccctcctag  ggcattgttg  accaggactg  
1981 agtctggaat  ctccaagtta  aagatggtga  atcaatgctt  cgggcttgga  gatggaacat  
2041 gcctcctctc  cattcagcta  gaaggaccaa  agcatgtggc  atttgatgg  ccagagtgcc  
2101 ctgaagcacc  actaccaacc  ttgcctcccc  ctctctcaa  agagcctctg  attgtgtcac  
2161 caaggggctc  acatcttatg  tctgccatgc  caggggtgtc  gccatccaga  tgtgttgaa  
2221 gcttccccct  ctgccttatg  ctcacctgtg  gacaccgagg  atgccctcac  attggtgctc  
2281 tctcctcatc  ctcagcccc  ctttgccaca  atggtatgat  ggcttggtag  cccctcgagg  
2341 cagatgcacc  tgacttgctg  ctattaaaaa  gccgtgtgcc  ttctaccaa  aaaaaaaaa  
2401 aaaa
```

//

[Disclaimer](#) | [Write to the Help Desk](#)
NCBI | NLM | NIH

Oct 4 2005 13:52:42





[\[Sign In\]](#)
[\[Register\]](#)

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Limits Preview/Index History Clipboard Details

Display **GenBank** Show **5** Send to

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

1: [AK025212](#). Reports Homo sapiens cDNA...[gi:10437679] [Links](#)

LOCUS	AK025212	1912 bp	mRNA	linear	PRI 13-SEP-2003
-------	----------	---------	------	--------	-----------------

DEFINITION Homo sapiens cDNA: FLJ21559 fis, clone COL06406.

ACCESSION AK025212

VERSION AK025212.1 GI:10437679

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM	Homo sapiens
----------	--------------

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1

AUTHORS Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y.,
Okamoto, S., Okitani, R., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T.,
Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1912)

AUTHORS Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,
Shibahara, T., Tanaka, T. and Nakamura, Y.

TITLE Direct Submission

JOURNAL Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)

COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).

```
FEATURES
    source                Location/Qualifiers
                        1..1912
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="COL06406"
                        /tissue_type="colon"
                        /clone_lib="COL"
                        /note="cloning vector pME18SFL3"
```

ORIGIN

1 atgatgcatc ttaaatacag gaggtacatg tatgtggcaa aaatggcaac atcttgtgaa
61 caacgctcatg attcaaactt gacggggaga ggagcagggg ggaaggtaac ctgcaccctg
121 acgtcttcag gggaggacac acaagcacc ctcaggtgg cctctcttga aaacccttgc

181 cccacgact ggcaccctgc tttccccatt cactgccttg tctccacccc tgcacctcct
241 tgctctcctg ccgctgactt tgggaccctt accctgcagg ctgtcctgga atctcctcgg
301 ggatgaggca gctgccgagc tggcccaggt gctgccgcag atgggcccgc tgaagagagt
361 ggagtatgag gggccggggg aggaatggga cgggctaaag ggggacctac atcccgggaa
421 caccaagagg ccaactgggtc agtccccctgc ctcccagaaa gcccttcctt gagttgcaca
481 ctctggcctg ttccaagccc ctgccaggct tagttccccc tgggttctag ccttcagcct
541 tcccgcctgca cctgccacca gtccccctgtt gtcttttggg ttccttgaga aggtagtgtg
601 ggagactgtg tccccctgacc ttggcctgag gaagggacct aggaaactct cacaccctt
661 ctcatggccg tgtttctctt tccccctccc tcaactgtcca ctgagaagcc tggagaagaa
721 tcagatcaca gctttggggg cctggctcct ggctgaagga ctggcccagg ggtctagcat
781 ccaagtcac cgcctctgga ataaccctat tccctgcgac atggcccagc acctgaagag
841 ccaggagccc aggtctggact ttgccttctt tgacaaccag cccagggccc cttggggtag
901 ttgatggccc cctcaagacc tttggaatcc agccagggtga tgcacccaaa tgatccacct
961 ttcgccact gggataaatg actcaggaaa gaagagcctc ggcagggcgc tctgcactcc
1021 acccaggagg aaggatacgt gtgtcctgct gcagtcctca gggagaactt ttttgggaac
1081 caggagctgg gtctggacaa aggagtacct tgcattacgt gggatatgtg tgatcaattg
1141 gggacatgcg acacacaatg aggggtgtcac gacaatgcat gacacgtacg gttatatgtg
1201 gcagtgtgac cccttgacat gtggcggttac atgaaagtca gtgtggcacg tgttctgtgg
1261 catgggtgct ggcaccccaa gtagcaggat acatgattgt tgggtctatat atgacacatg
1321 acaaagtgtc atgtcacagg actcatggct ggccagatga cctcaggctg gcccagatc
1381 taatttatta atttttaaag caaatacata tttatagatt gtgtgtatgg agcagctaag
1441 tcaggaaaag tcttcgccc gagctgggag gggagagtgt ccatgcactg accagtccag
1501 gggctcaagg gccagggtc tggacaagc cagggactca gccattaagt cccctcctgc
1561 ctcaatcctc agcctaccca tctataaact tgatgactcc tcccttactt acatactagc
1621 ttccaaggac aggtggagggt agggccagcc tggcgggagt ggagaagccc agtctgtcct
1681 atgtaaggga caaagccagg tctaattgta ctgggtaggg ggcactgcca agacaataag
1741 ctaggctact gggctccagct actactttgg tgggattcag gtgagtctcc atgcacttca
1801 catgttacct agtgttcttg ttacttccaa ggagaaccaa gaatggctct gtcacactcg
1861 aagccagggt tgatcaataa acacaatgggt attccaaaaa aaaaaaaaaa aa

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42




[\[Sign In\]](#)
[\[Register\]](#)

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Limits Preview/Index History Clipboard Details

Display **GenBank** Show **5** Send to

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: AK025362. Reports Homo sapiens cDNA...[gi:10437863]

Links

LOCUS AK025362 3495 bp mRNA linear PRI 13-SEP-2003

DEFINITION Homo sapiens cDNA: FLJ21709 fis, clone COL10077.

ACCESSION AK025362

VERSION AK025362.1 GI:10437863

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM	Homo sapiens
----------	--------------

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1

AUTHORS Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y.,
Okamoto, S., Okitani, R., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T.,
Shibahara, T., Tanaka, T., Nakamura, Y., Isoqai, T. and Sugano, S.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 3495)

AUTHORS Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,
Shibahara, T., Tanaka, T. and Nakamura, Y.

TITLE Direct Submission

JOURNAL Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)

COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).

```

FEATURES             Location/Qualifiers
     source            1..3495
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="COL10077"
                        /tissue_type="colon"
                        /clone_lib="COL"
                        /note="cloning vector pME18SFL3"
     CDS               205..>3495
                        /note="unnamed protein product"
                        /codon_start=1
                        /protein_id="BAB15120.1"

```

```
/db_xref="GI:10437864"  
/translation="MGPDGPGPVLTLFSLCNGTLLPGCRVMATSRPGKLPACLPAEA  
AMVHMLGFDGPRVEEYVNHFFSAQPSREGALVELQTNGRLRSLCAVPALCQVACLCLH  
HLLPDHAPGQSVALLPNMTQLYMQMVLALESPPGHLPTSSLLDLGEVALRGLETGKVI  
YAKDIAPPLIAFGATHSLLTSFCVCTGPGHQQTGYAFTHLSLQEFALAALHLMASPKVN  
KDTLTQYVTLHSRWVQRTKARLGLSDHLPTFLAGLASCTCRPFLSHLAQGNEDCVGAK  
QAAVVQVLKKLATRKLTPGKVVELCHCVDDETQEPELASLTAQSLPYQLPFHNFPLTCT  
DLATLTNILEHREAPIHLDFDGCPLPHCPEALVCGGQIENLSFKSRKCGDAFAEALS  
RSLPTMGRQLQMLGLAGSKITARGISHLVKALPLCPQLKEVSFRDNQLSDQVVLNIVEV  
LPHLPRLRKLDLSSNSICVSTLLCLARVAVTCPTVRMLQAREADLIFFLLSPPTETAE  
LQRAPDLQESDGQRKGAQSRSLTLRLQKCQLQVHDAEALIALLOEGPHLEEVLDLGNQ  
LEDEGCRMLMAEASQLHIARKLDLSDNGLSVAGVHCVLRAVSACWTLAELHISLQHKT  
VIFMFAQEPEEQKGPQERAAFLDSLMLQMPSELPLSSRRMRLTHCGLQEKHLEQLCKA  
LGGSCHLGHHLDFSGNALGDEGAARLAQLLPGLGALQSLNLSENGLSLDAVLGLVRC  
FSTLQWLFRLDISFESQHILLRGDKTSRDMWATGSLPDFPAAAKFLGFRQRCIPRSLC  
LSECPLEPPSLTRLCATLKDCPGPLELQLSCEFLSDQSLETLLDCLPQLSLQLS  
QTGLSPKSPFLLANTLSLCPRVKKVDLRSLHHATLHFRSNEEEEGVCCGFTGCSLSQE  
HVESLCWLLSKCKDLSQVDLSANLLGDSGLRCLLECLPQVPI SGLLDLSHNSISQESA  
LYLLETLPSCPRVREASVNLGSERSFRIHFSREDQAGKTLRLSECSFRPEHVSRLATG  
LSKSLQLTELTLTQCCLGQKQLAILLSLVGRPAGLFLSLRDSTRHTEKLSFPTLEACAL  
GFKKKKKKKK"
```

ORIGIN

```
1 caccatctga actgtttcca ggcctgttc ctttttgaat tccgccagct caacttgatc  
61 acgaggttcc tgacaccgtc cgagctcctt tttgatctgt acctgagccc tgaatcggac  
121 caccagactg tcttccagta cctggagaag aacgctgacc aagtcctgct gatctttgat  
181 gggctagatg aggccctcca gcctatgggt cctgatggcc caggcccagt cctcaccctt  
241 ttctcccatc tctgcaatgg gaccctcctg cctggctgcc gggatgatggc tacctcccgt  
301 ccagggaagc tgcctgcctg cctgcctgca gaggcagcca tgggtccacat gttgggcttt  
361 gatgggccac gggatgaaga atatgtgaat cacttcttca gcgccagcc atcgcgggag  
421 ggggccctgg tggagttaca gacaaatgga cgtctccgaa gcctgtgtgc ggtgcccgca  
481 ctgtgccaaag tcgcctgtct ctgcctccac catctgcttc ctgaccacgc cccaggccag  
541 tctgtggccc tctgcccac catgactcag ctctatatgc agatggtgct cgccctcagc  
601 cccctggggc acttgcccac ctgcctccca ctggacctgg gggaggtggc cctgaggggc  
661 ctggagacag ggaaggttat cttctatgca aaagatatg ctccaccctt gatagctttt  
721 ggggccactc acagcctgct gacttccttc tgcgtctgca caggccctgg gcaccagcag  
781 acaggctatg ctttcaccca cctcagcctg caggagtttc ttgctgccct gcacctgatg  
841 gccagcccca aggtgaacaa agacacactt acccagtatg ttaccctcca tccccgctgg  
901 gtacagcgga ccaaagctag actgggcctc tcagaccacc tccccacctt ctggcggggc  
961 ctggcatcct gcacctgccg ccccttcctt agccacctgg cgcagggcaa tggagctgtg  
1021 gtgggtgcca agcaggctgc tgtagtgcag gtgttgaaga agttggccac ccgcaagctc  
1081 acagggccaa aggttgtaga gctgtgtcac tgtgtggatg agacacagga gcctgagctg  
1141 gccagtctca ccgcacaaag cctcccctat caactgccct tccacaattt cccactgacc  
1201 tgcaccgacc tggccaccct gaccaacatc ctagagcaca gggaggcccc cateccacctg  
1261 gattttgatg gctgtccctt ggagcccac tgccctgagg ctctggtagg ctgtgggcag  
1321 atagagaatc tcagctttaa gagcaggaag tgtggggatg cctttgcaga agccctctcc  
1381 aggagcttgc cgacaatggg gaggctgcag atgctggggt tagcaggaag taaaatcact  
1441 gcccgaggca tcagccacct ggtgaaagct ttgcctctct gtccacagct gaaagaagtc  
1501 agttttcggg acaaccagct cagtgaccag gtggtgctga acattgtgga ggttctccct  
1561 cacctaccac ggctccgga gcttgacctg agcagcaaca gcatctgctg gtcaacccta  
1621 ctctgcttgg caaggggtggc agtcacgtgt cctaccgtca ggatgcttca ggccagggag  
1681 gcggacctca tcttcttctt tccccgccc acagagacaa ctgcagagct acaaagagct  
1741 ccagacctgc aggaaagtga cggccagagg aaaggggctc agagcagaag cttgacgctc  
1801 aggctgcaga agtgtcagct ccaggtccac gatgctggagg ccctcatagc cctgctccag  
1861 gaaggccctc acctggagga agtggaacct tcaggaacc agctggaaga tgaaggctgt  
1921 cggctgatgg cagaggctgc atcccagctg cacatcgcca ggaagctgga cctcagcgac  
1981 aacgggcttt ctgtggccgg ggtgcattgt gtgctgaggg ccgtgagtgc gtgctggacc  
2041 ctggcagagc tgcacatcag cctgcagcac aaaactgtga tcttcatgtt tgcccaggag  
2101 ccagaggagc agaagggggc ccaggagagg gctgcatttc ttgacagcct catgctccag  
2161 atgccctctg agctgcctct gagctcccga aggatgaggc tgacacattg tggcctccaa  
2221 gaaaagcacc tagagcagct ctgcaaggct ctgggaggaa gctgccacct cggtcacctc
```

2281 cacctcgact tctcaggcaa tgctctgggg gatgaaggtg cagcccggct ggctcagctg
2341 ctcccagggc tgggagctct gcagtccttg aacctcagtg agaacggttt gtccctggat
2401 gccgtgttgg gcttggttcg gtgcttctcc actctgcagt ggctcttccg cttggacatc
2461 agctttgaaa gccaacacat cctcctgaga ggggacaaga caagcaggga tatgtgggcc
2521 actggatctt tgccagactt cccagctgca gccaaagtct tagggttccg tcagcgtgc
2581 atccccagga gcctctgcct cagtgaagtgt cctctggagc cccaagcct caccgcctc
2641 tgtgccactc tgaaggactg cccgggaccc ctggaactgc aattgtcctg tgagttcctg
2701 agtgaccaga gcctggagac tctactggac tgcttacctc aactccctca gctgagcctg
2761 ctgcagctga gccagacggg actgtccccg aaaagccctt tcctgctggc caacacctta
2821 agcctgtgtc cacgggttaa aaaggtggat ctcaggtccc tgcaccatgc aactttgcac
2881 ttcagatcca acgaggagga ggaaggcgtg tgctgtgggt tcacaggctg cagcctcagc
2941 caggagcacg tagagtcact ctgctggttg ctgagcaagt gtaaagacct cagccagggtg
3001 gatctctcag caaacctgct gggcgacagc ggactcagat gccttctgga atgtctgccg
3061 caggtgccca tctccggttt gcttgatctg agtcacaaca gcatttctca ggaaagtgcc
3121 ctgtacctgc tggagacact gccctcctgc ccacgtgtcc gggaggcctc agtgaacctg
3181 ggctctgagc ggagcttccg gattcacttc tccagagagg accaggctgg gaagacactc
3241 aggctaagtg agtgcagctt ccggccagag cacgtgtcca ggctggccac cggcttgagc
3301 aagtccctgc agctgacgga gctcacgctg acccagtgtg gcctgggcca gaagcagctg
3361 gccatcctcc tgagcctggg ggggcgaccc gcagggtgt tcagcctcag agactccaca
3421 aggcacacag agaaactgtc cttccccaca ctggaggcct gtgctttggg atttaagaaa
3481 aaaaaaaaaa aaaaa

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42



My NCBI
[Sign In]
[Register]

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books
Search for

Limits Preview/Index History Clipboard Details

Display Show Send to

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [AK027416](#). Reports Homo sapiens cDNA...[gi:14042077]

[Links](#)

LOCUS AK027416 3308 bp mRNA linear PRI 30-JAN-2004
DEFINITION Homo sapiens cDNA FLJ14510 fis, clone NT2RM1000623, weakly similar to RIBONUCLEASE INHIBITOR.
ACCESSION AK027416
VERSION AK027416.1 GI:14042077
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.
TITLE Complete sequencing and characterization of 21,243 full-length human cDNAs
JOURNAL Nat. Genet. 36 (1), 40-45 (2004)
PUBMED [14702039](#)

REFERENCE 2
 AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
 Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
 Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
 Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
 Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,
 Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
 Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.

TITLE NEDO human cDNA sequencing project
 JOURNAL Unpublished

REFERENCE 3 (bases 1 to 3308)
 AUTHORS Isogai,T. and Otsuki,T.
 TITLE Direct Submission
 JOURNAL Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
 Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology; cDNA library construction,
 5'- & 3'-end one pass sequencing and clone selection: Helix
 Research Institute (supported by Japan Key Technology Center etc.)
 and Department of Virology, Institute of Medical Science,
 University of Tokyo.

FEATURES Location/Qualifiers
 source 1..3308
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="NT2RM1000623"
 /cell_line="NT2"
 /cell_type="teratocarcinoma"
 /clone_lib="NT2RM1"
 /note="cloning vector: pUC19FL3
 mRNA from uninduced NT2 neuronal precursor cells."
 CDS 56..2317
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="BAB55098.1"
 /db_xref="GI:14042078"
 /translation="MWATGSLPDFPAAKFLGFRQRCIPRSLCLSECPLEPPSLTRLC
 ATLKDCPGPLELQLSCEFLSDQSLETLLDCLPQLPQLSLLQLSQTGLSPKSPFLLANT
 LSLCPRVKKVDLRLSHHATLHFRSNEEEEGVCCGLSANLLGDSGLRCLLECLPQVPIS
 GLLDLSHNSISQESALYLLETLPSCPRVREASVNLGSEQSFRIHFSREDQAGKTLRLS
 ECSFRPEHVSRLATGLSKSLQLTELTLTQCCLGQKQLAILLSLVGRPAGLFSRLVQEP
 WADRARVLSLLEVCAQASGSVAEISISSETQQQLCVQLEFPQREENPEAVALRLAHCDL
 GAHHSLLVGQLMETCARLQQLSLSQVNLCEDDDASSLLQLSLLLSLSELKTFRLTSSC
 VSTEGLAHLASGLGHCHHLEELDLSNNQFDEEGTKALMRALEGKMWMLKRLDLSHLLLN
 SSTLALLTHRLSQMTCLQSLRLNRNSIGDVGCHLSEALRAATSLEELDLSHNQIGDA
 GVQHLATILPGLPELRKIDLSGNSISSAGGVQLAESLVLCCRLEELMLGCNALGDPTA
 LGLAQELPQHRLRVLHLPFSLHLPGLGPGGALSQAALDGFPHLEEISLAENNLAGGVLRFCM
 ELPLLRQIDLVSKIDNQTAKLTTSSFTSCPALEVILLSWNLLGDEAAAEALQVLPQM
 GRLKRVDPKQNQITALGAWLLAEGLAQGSSIQVIRLWNNPIPCDMAQHLKSQEPRLDF
 AFFDNQPQAPWGT"


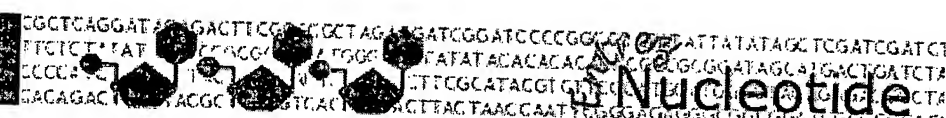
ORIGIN
 1 catcagcttt gaaagccaac acatcctcct gagaggggac aagacaagca gggatatgtg
 61 ggccactgga tctttgccag acttcccggc tgcagccaag ttcttagggg tccgtcagcg
 121 ctgcatcccc aggagcctct gcctcagtga gtgtcctctg gagcccccaa gcttcacccg
 181 cctctgtgcc actctgaagg actgcccggg acccctggaa ctgcaattgt cctgtgagtt
 241 cctgagtgc cagagcctgg agactctact ggactgctta cctcaactcc ctcagctgag
 301 cctgctgcag ctgagccaga cgggactgtc cccgaaaagc cccttctctgc tggccaacac

```
361 cttaagcctg tgtccacggg ttaaaaaggt ggatctcagg tccctgcacc atgcaacttt
421 gcaattcaga tccaacgagg aggaggaagg cgtgtgctgt ggtctctcag caaacctgct
481 gggcgacagc ggactcagat gccttctgga atgtctgccg caggtgccc a tctccggttt
541 gcttgatctg agtcacaaca gcatttctca ggaaagtgcc ctgtacctgc tggagacact
601 gccctcctgc ccacgtgtcc gggaggcctc agtgaacctg ggctctgagc agagcttccg
661 gattcacttc tccagagagg accaggctgg gaagacactc aggctaagt agtgcagctt
721 ccggccagag cacgtgtcca ggctggccac cggcttgagc aagtcctgc agctgacgga
781 gctcacgctg acccagtgtc gcctgggcca gaagcagctg gccatcctcc tgagcttggg
841 ggggagaccc gcagggtgt tcaagtctcag ggtgcaggag ccgtgggagg acagagccag
901 gggtctctcc ctggttagaag tctgcgccc ggctcaggc agtgtcgtg aaatcagcat
961 ctccgagacc cagcagcagc tctgtgtcca gctggaattt cctcgccagg aagagaatcc
1021 agaagctgtg gcaactcagg tggtcactg tgacctgga gccaccaca gccttcttgt
1081 cgggcagctg atggagacat gtgccaggct gcagcagctc agcttgtctc aggttaacct
1141 ctgtgaggac gatgatgcca gttccctgct gctgcagagc ctctgtgtt cctctctga
1201 gctgaagaca tttcggctga cctccagctg tgtgagcacc gagggcctcg cccacctggc
1261 atctggctg ggcactgcc accacttga ggagctggac ttgtctaaca tcaatttga
1321 tgaggagggg accaaggcgc tgatgagggc ccttgagggg aaatggatgc taaagaggct
1381 ggacctcagt caccttctgc tgaacagctc caccttggcc ttgcttactc acagactaag
1441 ccagatgacc tgcctgcaga gcctcagact gaacaggaa agtatcgggt atgtcgggtg
1501 ctgccacctt tctgaggctc tcagggtgtc caccagccta gaggagctgg acttgagcca
1561 caaccagatt ggagacgtg gtgtccagca cttagctacc atcctgcctg ggctgccaga
1621 gctcaggaag atagacctct cagggaatag catcagctca gccgggggag tgcagttggc
1681 agagtctctc gttctttgca ggcgcctgga ggagtgtatg cttggctgca atgccctggg
1741 ggatcccaca gccctggggc tggctcagga gctgccccag cacctgaggg tctacacct
1801 accattcagc catctggggc caggtggggc cctgagcctg gccaggccc tggatggatt
1861 cccccatttg gaagagatca gcttggcggg aaacaacctg gctggagggg tctgcgttt
1921 ctgtatggag ctcccgtgc tcagacagat agacctggtt tcctgtaaga ttgacaacca
1981 gactgccaa gctcctcacct ccagcttcac gagctgccct gccctggaag taatcttgtc
2041 gtccctggaat ctcctcgggg atgaggcagc tgccgagctg gccaggtgc tgccgcagat
2101 gggccggctg aagagagtgg acccgagaaa gaatcagatc acagctttgg gggcctggct
2161 cctggtgaa ggactggccc aggggtctag catccaagtc atccgcctct ggaataaacc
2221 cattccctgc gacatggccc agcacctgaa gagccaggag cccaggctgg actttgcctt
2281 ctttgacaac cagccccagg ccccttgggg tacttgatgg cccctcaag acctttggaa
2341 tccagccaag tgatgcaccc aaatgatcca ctttcgccc actgggataa atgactcagg
2401 aaagaagagc ctccggcagg cgctctgcac tccaccagg aggaaggata cgtgtgtcct
2461 gctgcagtcc tcaggagaaa cttttttggg aaccaggagc tgggtctgga caaaggagta
2521 ccctgcatta cgtgggatat gtgtgatcaa ttggggacat gcgacacaca atgagggtgt
2581 catgacaatg catgacacgt acggttatat gtggcagtg gaccttga catgtggcgt
2641 tacatgaaag tcagtgtggc acgtgttctg tggcatgggt gctggcatcc caagtggcag
2701 gatacatgat tgttgggtcta tatatgacac atgacaaatg tccatgtcac aggactcatg
2761 gctggccaga tgacctcagg ctggcccaa atctaattta ttaattttta aagcaaatac
2821 atatttatag attgtgtgta tggagcagct aagtcaggaa aagtcctccg cccgagctgg
2881 gaggggagag tgtccatgca ctgaccagtc caggggctca agggccagg ctctggaaca
2941 agccagggac tcagccatta agtccccctc tgccctcaat ctcagcctac ccatctataa
3001 acttgatgac tcctccctta cttacatact agcttccaag gacaggtgga ggtagggccca
3061 gcctggcggg agtgagaga cccagtctgt cctatgtaag ggacaaagcc aggtctaattg
3121 gtactgggta gggggcactg ccaagacaat aagctaggct actgggtcca gctactactt
3181 tgggtgggatt caggtgagtc tccatgcact tcacatgtta cccagtgttc ttgttacttc
3241 caaggagaa caagaatggc tctgtcacac tcgaagccag gtttgatcaa taaacacaat
3301 ggtattcc
```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42

[PubMed](#)
[Nucleotide](#)
[Protein](#)
[Genome](#)
[Structure](#)
[PMC](#)
[Taxonomy](#)
[OMIM](#)
[Books](#)

Search for

Display

Range: from to ☐ Reverse complemented strand

Features: ☐ SNP ☐ CDD ☒

☐ 1: [AK074109](#). Reports Homo sapiens mRNA...[gi:18676565]

[Links](#)

LOCUS AK074109 4287 bp mRNA linear PRI 15-FEB-2002
 DEFINITION Homo sapiens mRNA for FLJ00180 protein.
 ACCESSION AK074109
 VERSION AK074109.1 GI:18676565
 KEYWORDS fis (full insert sequence).
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1
 AUTHORS Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.
 TITLE The nucleotide sequence of a long cDNA clone isolated from human spleen
 JOURNAL Published Only in Database (2002)

REFERENCE 2 (bases 1 to 4287)
 AUTHORS Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.
 TITLE Direct Submission
 JOURNAL Submitted (21-JAN-2002) Takahiro Nagase, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/NEDO, Tel:81-438-52-3913, Fax:81-438-52-3914)

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert and 5'- & 3'-end one pass sequencing: Research Association for Biotechnology; cDNA library construction and clone selection: Kazusa DNA Research Institute.

FEATURES
 source Location/Qualifiers
 1..4287
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="FLJ00180"
 /tissue_type="spleen"
 /dev_stage="adult"
 /note="vector:pBluescriptII SK plus"

gene 1..4287
 /gene="FLJ00180"

CDS <1..1500
 /gene="FLJ00180"
 /inference="non-experimental evidence, no additional details recorded"
 /note="Start codon is not identified."
 /codon_start=1

/product="FLJ00180 protein"
/protein_id="BAB84935.1"
/db_xref="GI:18676566"
/translation="VLHCLHELQHTELARSVEEAMESGALARLTGPAHRAALAYLLQV
SDACAEANLSLSLSQGVLSLLPQLLYCRKLRLDTNQFQDPVMELLGSVLSGKDCRI
QKISLAENQISNKGAKALARSLLVNRSLTSLDLRGNSIGPQAKALADALKINRTLTS
LSLQGNTRVDDGARSMAEALASNRTLMLHLQKNSIGPMGAQRMADALKQNRSLKELM
FSSNSIGDGGAKALAEALKVNQGLSGLDLQNSISDAGVAALMGALCTNQTLTSLSLR
ENSISPEGAQAIAHALCANSTLKNLDLTANLLHDQGARAIAVAVRENRTLTLHLQWN
FIQAGAAQALGQALQLNRSLTSLDLQENAIGDDGACAVARALKVNTALTALYLQVASI
GASGAQVLGEALAVNRTLEILDLRGNAIGVAGAKALANALKVNSSLRRLNLQENSLGM
DGAICITATALSGNHRLQHINLQGNHIGDSGARMISEAIKTNAPTCTVEM"

ORIGIN


```
1  gtgttgcaact  gcctgcatga  gctgcagcac  accgagctgg  cccgcagcgt  ggaggaggcc
61  atggagagcg  gggccctggc  caggctgact  ggtcccgcgc  accgcgctgc  cctggcctac
121  ctcttgcaag  tgtccgacgc  ctgtgccagc  gaggccaacc  tgtccctgag  cctcagccag
181  ggcgtccttc  agagcctgct  gcccagctg  ctctactgcc  ggaagctcag  gctggacacc
241  aaccagttcc  aggaccccg  gatggagctg  ctgggcagcg  tgctgagtgg  gaaggactgt
301  cgcattcaga  agatcagctt  ggcggagaac  cagatcagta  acaaaggggc  caaagctctg
361  gccagatccc  tcttggtcaa  cagaagtctg  acctctctgg  acctccgcgg  taactccatt
421  ggaccacaag  gggccaaggc  gctggcagac  gctttgaaga  tcaaccgcac  cctgacctcc
481  ctgagcctcc  agggcaacac  cgttagggat  gatggtgcca  ggtccatggc  tgaggccttg
541  gcctccaacc  ggacctctc  catgctgcac  ctgcagaaga  acagcatcgg  gcccatggga
601  gccagcgga  tggcagatgc  cttgaagcag  aacaggagtc  tgaaagagct  catgttctcc
661  agtaatagta  ttggtgatgg  aggtgccaa  gccctggctg  aggccctgaa  ggtgaaccag
721  ggcctggaga  gcctggacct  gcagagcaat  tccatcagtg  acgcaggagt  ggcagcactg
781  atggggggcc  tctgcaccaa  ccagaccctc  ctccagctca  gccttcgaga  aaactccatc
841  agtcccagg  gagcccaggc  catcgctcat  gccctctgcg  ccaacagcac  cctgaagaac
901  ctggacctga  cagccaacct  cctccacgac  cagggtgccc  gggccatcgc  agtggcagtg
961  agagaaaacc  gcacctcac  ctcccttcac  ctgcagtgg  acttcatcca  ggccggcgct
1021  gccaggccc  tgggacaagc  actacagctc  aacaggagcc  tcaccagctt  agatttacag
1081  gagaacgcca  tcggggatga  cggagcgtgt  gcggtggccc  gtgcactgaa  ggtcaacaca
1141  gccctcactg  ctctctatct  ccagggtggc  tcaattggtg  cttcaggcgc  ccagggtgta
1201  ggggaagcct  tggctgtgaa  cagaaccttg  gagattctcg  acttaagagg  aaatgccatt
1261  ggggtggctg  gagccaaagc  cctggcaaat  gctctgaagg  taaactcaag  tctccggaga
1321  ctcaatcttc  aagagaattc  tctggggatg  gacggggcga  tatgcattgc  cacagcactg
1381  tctggaaacc  acaggctcca  gcatatcaat  ctccaggga  accacattgg  ggactccggg
1441  gccaggatga  tctcagaggc  catcaagaca  aatgctccca  cgtgcactgt  tgaaatgtga
1501  tcctggtgga  cggatcagga  gaatgggcag  atgctcagct  ggaagctttt  gaacagaaag
1561  gccgacttct  ggggggcctg  tctgggagct  gggaaacgtg  cttgctcagc  acgagagccg
1621  ggctctgcag  ggaggaagga  gagtgctgc  cggaggaggt  cgtgagctcc  tcttctgctg
1681  caggagtgg  ccaggcagg  ggtgacgggt  actctgttat  ggcacagaga  agggaggggc
1741  ccccccaag  ggactagggt  ccaaaggcct  gaaagctgag  cagtacagga  ggctggttcc
1801  agcttttac  cctgaggact  tcatgtgtcc  ccaaccttta  aaaatgttta  ttactgcccc
1861  tttccactca  cctggttaaa  aatcatccca  tgctctgaga  tgagctgcca  cctcaagccc
1921  gtgaggagca  tccgtttggt  aggggttaaca  gaggggaccc  ttctttatct  ttcaagaag
1981  aagatttcag  ggtatcatcc  ttacagacat  gaaaaagcta  tgggaaaatt  gtgaagataa
2041  atgaaagttt  taattctagg  attctggaaa  cagagacagt  aagagttctc  caaggatttt
2101  gccttttttg  tttgtttttg  agatggagtc  tcgctcttgt  cgccaggct  ggagtgcagt
2161  ggcacgatct  cagctccctg  caacctccgc  ctcccgggtt  catgtgatcc  tcctgcctca
2221  gcctccccag  tagctgggaa  tacaggcacc  cgccaccatg  cccggctaatt  tttttagtct
2281  ttagtagaga  cgggggttca  tcatgttggc  caggctggtc  tcgaactcct  gacctcaggt
2341  gatccatcag  cctgggcctc  ccaaagtact  gggattacag  gcatgagcca  ccacacctgg
2401  cccattttt  tattttattac  aaaatcaaag  acatgggtga  tgcttgccac  atgttgtctg
2461  gagtctggca  cactggttat  caatagcaca  ttcagtgtat  tcagtgtatg  cattctttat
2521  ttatttttga  gacagaatct  gtcacccagg  ctggagtgc  gtggcatgat  ctcagctcac
2581  tgtaggctct  acctcatggt  ttccagtgat  tctcctgcct  cggcctccca  agtagttggg
2641  tctacaggca  cgcaccacca  caccagcta  atttttgtat  ttttagtaga  gatgggggtt
2701  caccatgttg  atcaggctgg  tctttaactc  ctgacctcaa  gtgatccacc  cacctcagcc
2761  tcccaaagtg  ctgggattac  aggtgtgagc  cactgcacct  ggcagtgatg  tcattcctta
```

2821 ctaggcttcc aaagccactg ctgtggccac agcttccatg gagacaggca agctgagcct
2881 ctatgtggca ccaattcctg cagctgtttg tggtggaggg aaaaaaatcc aaatggacat
2941 caacagcttt catcaactaa ataaccacag aaaatattta tgaagactat aaagcaatga
3001 ttacttttga attggaaagg aatcactatt atttgaaatg tttcttcaaa agtgagcatc
3061 cagacaggaa ccatcatgga tgctgaggcc atggatgaag gcctactcgg gaagatgata
3121 tccttgcagt ctcaaaacgg caccacacaa aggtgatatc ctaatttaca aagggaacaa
3181 ggtaccttaa tctgaaatct ggcaaatgca gcctcaacag aagtgcaga attgaacatc
3241 gccataatg ggacacacag acatcacatg cccccagtct gatgcaccac ggagtcgtct
3301 ctgatgtatt cttgtcaaaa aatgtttgcc tgattctaata catgaaagaa caattagaaa
3361 aaatccaaat tgacagatat tctgcagaat aaatggcctg acctcatcaa aaacatcaat
3421 gtcataaaaa acacaaaaaa ttgcagatag cgtgaaatta aagattacag agatataact
3481 taatgcaaga tctctgactg gatcctagac tgcaggaaaa agtctgctat aaagaacatt
3541 tggatcactt gtagtagctg ggaaataaaa caaaacatta tttgtaaaag gggggaaatc
3601 tgaacatggg tcttgcagta tttatgacag tttttgcggg gcagagattt ctagattgac
3661 agctgtttta gtactttcaa ggtgatgctc tgtctgctgg tttgcattgt ttctgtctga
3721 gttaagagac tggcagaaca cagagttgca gtagccaaac actggagaaa gctgggccct
3781 acagaaacct aacgctgaag aaacctcagg agccaaactg gtggagaaaa caaagagtcc
3841 tccctctctc ccttttcaaa taatgatcat acatcttcaa gctgtctgaa atggttaagg
3901 agttcagttc gtcgtcaggc acacaccaga gccagctagc ccacacagac cccatcagag
3961 caaaacagac aagagaattt aattcatatc cacatagaaa ggacttctag gtaggaggta
4021 gacccttttag ctcccttcca attaaaggag tccccaattc tggcacctga gagtccctg
4081 ggtctaacag ctatgatatt tatgtagtgt gttgcttacc taaatgaata caatttcctt
4141 ccagacacgt gacactgata ttaaagtgtc aatgagaggg atctatttct tcttgtacgc
4201 taaaagagaa acagcagttc agatttccca tcagaagtcc gaggactttg ttcttgataa
4261 ctactaccaa taaaattga gtatttg

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42



CGCTCAGGATAGGACTTCCTGCTAGAGGATGGATCCCGGGCGCTTTATTATATAGCTCGATCGATCT
TTCTCTATATCTCCGCGCATGGGATATATACACACACAGCCGCGGATAGCAAGACTGATCTTA
LLCCATCT
CAGAGACT

Nucleotide

My NCBI
[\[Sign In\]](#)
[\[Register\]](#)

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Limits Preview/Index History Clipboard Details

Display Show Send to

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [AK074133](#). Reports Homo sapiens mRNA...[gi:18676613]

[Links](#)

LOCUS AK074133 4121 bp mRNA linear PRI 15-FEB-2002

DEFINITION Homo sapiens mRNA for FLJ00206 protein.

ACCESSION AK074133

VERSION AK074133.1 GI:18676613

KEYWORDS fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1

AUTHORS Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.

TITLE The nucleotide sequence of a long cDNA clone isolated from human spleen

JOURNAL Published Only in Database (2002)

REFERENCE 2 (bases 1 to 4121)

AUTHORS Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.

TITLE Direct Submission

JOURNAL Submitted (21-JAN-2002) Takahiro Nagase, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/NEDO, Tel:81-438-52-3913, Fax:81-438-52-3914)

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert and 5'- & 3'-end one pass sequencing: Research Association for Biotechnology; cDNA library construction and clone selection: Kazusa DNA Research Institute.

FEATURES Location/Qualifiers

source 1..4121
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="FLJ00206"
/tissue_type="spleen"
/dev_stage="adult"
/note="vector:pBluescriptII SK plus"

gene 1..4121
/gene="FLJ00206"

CDS <1..2109
/gene="FLJ00206"
/inference="non-experimental evidence, no additional details recorded"
/note="Start codon is not identified."
/codon_start=1

```
/product="FLJ00206 protein"  
/protein_id="BAB84959.1"  
/db_xref="GI:18676614"  
/translation="QKCQLQVHDAEALIALLQEGPHLEEVDLSGNQLEDEGCRLMAEA  
ASQLHIARKLDLSDNGLSVAGVHCVLRAVSACWTLAELHISLQHKTVIFMFAQEPEEQ  
KGPQERAAFLDSLMLQMPSELPLSSRRMRLTHCGLQEKHLEQLCKALGGSCHLGHLL  
DFSGNALGDEGAARLAQLLPGLGALQSLNLSENGLSLDAVLGLVRCFSTLQWLFRLLDI  
SFESQHILLRGDKTSRDMWATGSLPDFPAAAKFLGFRKRCIPRSLCLSECPLEPPSLT  
RLCATLKDCPGPLELQLSCEFLSDQSLETLLDCLPQLPQLSLLQLSQTGLSPKSPFLL  
ANTLSLCPRVKKVDLRSLLHATLHFRSNEEEEGVCCGRFTGCSLSQEHVESLCWLLSK  
CKDLSQVDLSANLLGDSGLRCLLECLPQVPI SGLLDLSHNSISQESALYLLETLPSCP  
RVREASVNLGSEQSFRIHFSREDQAGKTLRLSECSFRPEHVSRLATGLSKSLQLTELT  
LTQCCLGQKQLAILLSLVGRPAGLFSRLRVQEPWADRARVLSLLEVCAQASGSVTEISI  
SETQQQLCVQLEFPQREENPEAVALRLAHCDLGAHHSLLVGQLMETCARLQQLSLSQV  
NLCEDDDDASSLLLQSLLLSLSELKTFRIQSSQDPGRLLPDLPLFPDHPQADLQLCEHRG  
PRPPGIWSGPLPPLGGAGLV"
```

ORIGIN



```
1  cagaagtgtc agctccaggt ccacgatgcg gaggccctca tagccctgct ccaggaaggg  
61  cctcacctgg aggaagtgga cctctcaggg aaccagctgg aagatgaagg ctgtcggtcg  
121 atggcagagg ctgcatccca gctgcacatc gccaggaagc tggacctcag tgacaacggg  
181 ctttctgtgg ccggggtgca ttgtgtgctg agggcctgta gtgcgtgctg gaccctggca  
241 gagctgcaca tcagcctgca gcacaaaact gtgatcttca tgtttgccc ggagccagag  
301 gagcagaagg ggccccagga gagggtgca tttcttgaca gcctcatgct ccagatgccc  
361 tctgagctgc ctctgagctc ccgaaggatg aggtgacac attgtggcct ccaagaaaag  
421 cacctagagc agctctgcaa ggctctggga ggaagctgcc acctcggta cctccacctc  
481 gacttctcag gcaatgctct ggggatgaa ggtgcagccc ggctggctca gctgctccca  
541 gggctgggag ctctgcagtc cttgaacctc agtgagaacg gtttgtccct ggatgccgtg  
601 ttgggtttgg ttcggtgctt ctccactctg cagtggctct tccgcttgga catcagcttt  
661 gaaagccaac acatcctcct gagaggggac aagacaagca gggatatgtg ggccactgga  
721 tctttgccag acttcccagc tgcagccaag ttcttagggg tccgtaagcg ctgcatcccc  
781 aggagcctct gcctcagtga gtgtcctctg gagcccccaa gcctcaccgg cctctgtgcc  
841 actctgaagg actgcccggg acccctggaa ctgcaattgt cctgtgagtt cctgagtgac  
901 cagagcctgg agactctact ggactgctta cctcaactcc ctgagctgag cctgctgcag  
961 ctgagccaga cgggactgtc cccgaaaagc cccttcctgc tggccaacac cttaagcctg  
1021 tgtccacggg ttaaaaaggt ggatctcagg tccctgcacc atgcaacttt gcacttcaga  
1081 tccaacgagg aggaggaagg cgtgtgctgt ggcagggtca caggctgcag cctcagccag  
1141 gagcacgtag agtcactctg ctggttgctg agcaagtgtg aagacctcag ccagggtgat  
1201 ctctcagcaa acctgctggg cgacagcgga ctgagatgcc ttctggaatg tctgcccgag  
1261 gtgcccactc ccggtttgct tgactgagtg cacaacagca tttctcagga aagtgccttg  
1321 tacctgctgg agacactgcc ctctgccca cgtgtccggg aggcctcagt gaactcgggc  
1381 tctgagcaga gcttccggat tcacttctcc agagaggacc aggctgggaa gacactcagg  
1441 ctaagtgagt gcagcttccg gccagagcac gtgtccaggc tggccaccgg cttgagcaag  
1501 tccctgcagc tgacggagct cacgctgacc cagtgtgcc tgggccagaa gcagctggcc  
1561 atcctcctga gcttggtggg gcgaccgcga gggctgttca gcctcagggt gcaggagccg  
1621 tgggcgga ca gagccagggt tctctccctg ttagaagtct gcgcccaggc ctcaggcagt  
1681 gtcactgaaa tcagcatctc cgagaccag cagcagctct gtgtccagct ggaatttctt  
1741 cgccaggaag agaatccaga agctgtggca ctcagggttg ctcactgtga ccttgagacc  
1801 caccacagcc ttcttgctcg gcagctgatg gagacatgtg ccaggctgca gcagctcagc  
1861 ttgtctcagg ttaacctctg tgaggacgat gatgccagtt cctgctgct gcagagcctc  
1921 ctgctgtccc tctctgagct gaagacattt cgcattcaga gctcccaaga cccagggcgg  
1981 ctctgctg acctgttgcc ctttgacccc caccaggctg acctccagct gtgtgagcac  
2041 cgagggcctc gccacactgg catctggtct gggccactgc caccacttg aggagctgga  
2101 cttgtctaac aatcaatttg atgaggaggg caccaaggcg ctgatgaggg cccttgaggg  
2161 gaaatggatg cttaaaggagc tggacctcag tcacctctg ctgaacagct ccaccttggc  
2221 cttgcttact cacagactaa gccagatgac ctgcctgcag agcctcagac tgaacaggaa  
2281 cagtatcggt gatgtcggtt gctgccacct ttctgaggct ctcagggtcg ccaccagcct  
2341 agaggagctg gacttgagcc acaaccagat tggagatgct ggtgtccagc acttagctac  
2401 catcctgcct gggctgccag agctcaggaa gatagacctc tcagggaata gcatcagctc  
2461 agccggggga gtgcagttgg cagagtctct cgttctttgc aggcgcctgg aggagttgat  
2521 gcttggtgctc aatgccctgg gggatcccac agccctgggg ctggctcagg agctgcccc
```

2581 gcacctgagg gtcctacacc taccattcag ccattctgggc ccaggtgggg ccttgagcct
2641 ggcccaggcc ctggatggat ccccccattt ggaagagatc agcttggcgg aaaacaacct
2701 ggctggaggg gtcctgcgtt tctgtatgga gctcccgtg ctcagacaga tagacctggt
2761 ttcctgtaag attgacaacc agactgccaa gtcctcacc tccagcttca cgagctgccc
2821 tgccctggaa gtaatcttgc tgcctggaa tctcctcggg gatgaggcag ctgccgagct
2881 ggcccagggtg ctgccgcaga tgggccggct gaagagagt gacctggaga agaatacagat
2941 cacagctttg ggggcctggc tcctggctga aggactggcc caggggtcta gcatccaagt
3001 catccgcctc tgggaataacc ccattccctg cgacatggcc cagcacctga agagccagga
3061 gcccgaggctg gactttgcct tctttgacaa ccagccccag gcccttggg gtacttgatg
3121 gcccctcaa gacctttgga atccagccaa gtgatgcacc caaatgatcc acctttcgcc
3181 cactgggata aatgactcag gaaagaagag ctcgggcagg gcgctctgca ctccaccag
3241 gaggaaggat acgtgtgtcc tgctgcagtc ctcagggaga acttttttgg gaaccaggag
3301 ctgggtctgg acaaaggagt accctgcatt acgtgggata tgtgtgatca attggggaca
3361 tgcgacacac aatgagggtg tcatgacaat gcatgacacg tacggttata tgtggcagtg
3421 tgacccttg acatgtggcg ttacatgaaa gtcagtgtgg cacgtgttct gtggcatggg
3481 tgctggcatc ccaagtagca ggatacatga ttgttggctc atatatgaca catgacaaat
3541 gtccatgtca caggactcat ggctggccag atgacctcag gctggcccaa gatctaattt
3601 attaattttt aaagcaaata catatttata gattgtgtgt atggagcagc taagtcagga
3661 aaagtcttcc gcccgagctg ggaggggaga gtgtccatgc actgaccagt ccaggggctc
3721 aagggccagg gctctggaac aagccaggga ctcagccatt aagtccttc ctgcctcaat
3781 cctcagccta cccatctata aacttgatga ctctccctt acttacatac tagcttccaa
3841 ggacaggtgg aggtagggcc agcctggcgg gaggggagaa gccagctctg tcctatgtaa
3901 gggacaaagc caggtctaata ggtactgggt agggggcact gccaagacaa taagctaggc
3961 tactgggtcc agctactact ttggtgggat tcaggtgagt ctccatgcac ttcacatgtt
4021 acccagtggt cttgttactt ccaaggagaa ccaagaatgg ctctgtcaca ctggaagcca
4081 ggtttgatca ataaacacaa tggatttcca cgtctagcgt g

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42

PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	OMIM	Books
--------	------------	---------	--------	-----------	-----	----------	------	-------

Search for

Limits Preview/Index History Clipboard Details

Display **GenBank** Show **5** Send to

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

1: [AK074182](#). Reports Homo sapiens mRNA...[gi:18676711]

Links

LOCUS AK074182 . 4520 bp mRNA linear PRI 15-FEB-2002

DEFINITION Homo sapiens mRNA for FLJ00255 protein.

ACCESSION AK074182

VERSION AK074182.1 GI:18676711

KEYWORDS fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1

AUTHORS Jikuya, H., Takano, J., Nomura, N., Kikuno, R., Nagase, T. and Ohara, O.

TITLE The nucleotide sequence of a long cDNA clone isolated from human spleen

JOURNAL Published Only in Database (2002)

REFERENCE 2 (bases 1 to 4520)

AUTHORS Jikuya, H., Takano, J., Nomura, N., Kikuno, R., Nagase, T. and Ohara, O.

TITLE Direct Submission

JOURNAL Submitted (21-JAN-2002) Takahiro Nagase, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:<http://www.kazusa.or.jp/NEDO>, Tel:81-438-52-3913, Fax:81-438-52-3914)

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert and 5'- & 3'-end one pass sequencing: Research Association for Biotechnology; cDNA library construction and clone selection: Kazusa DNA Research Institute.

FEATURES	Location/Qualifiers
source	1..4520 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon: <u>9606</u> " /clone="FLJ00255" /tissue_type="spleen" /dev_stage="adult" /note="vector:pBluescriptII SK plus"

```
gene      1..4520
          /gene="FLJ00255"
```

```
CDS          <102..2303
              /gene="FLJ00255"
              /inference="non-experimental evidence, no additional
              details recorded"
              /note="Start codon is not identified."
              /codon start=1
```

```
/product="FLJ00255 protein"  
/protein_id="BAB85008.1"  
/db_xref="GI:18676712"  
/translation="STYHERGDQGWLLMDPVGLQLGNKNLWSQLVRLLTKDPEWLNNAK  
MKFFLPNTDLDSRNETLDPEQRVILQLNKLHVQSDTWQSFHICVCMQLEVLPLDLEVL  
LLSTFGYDDGFTSQLGAEGKSQPESQLHHGLKRPHQSCGSSPRRKQCKKQOLELAKKY  
LQLLR TSAQQRYRSQIPGSGQPHAFHQVYVPPILRRATASLDTPEGAIMGDVKVEDGA  
DVSISDLFNTRVNKGPRVTVLLGKAGMGKTTLAHRLCQKWAEGHLNCFQALFLFEFRQ  
LNLITRFLTPSELLFDLYLSPESDHDTVFQYLEKNADQVLLIFDGLDEALQPMGPDGP  
GPVLTFLSHLCNGTLLPGCRVMATSRPGKLPACLPAAEAMVHMLGFDGPRVEEYVNHF  
FSAQPSREGALVELQTNGRLRSLCAVPALCQVACLCLHLLLPDHAPGQSVALLPNMTQ  
LYMQMVLALSPPGHLPTSSLLDLGEVALRGLGTGKVI FYAKDIAPPLIAFGATHSLLT  
SFCVCTGPGHQQTGYAFTHLSLQEFLLAALHLMASPKVNKDTLTQYVTLHSRWVQRTKA  
RLGLSDHLPTFLAGLASCTCRPFLSHLAQGNEDCVGAKQAAVVQVLKKLATRKLTGPK  
VVELCHCVDETQEPELASLTAQSLPYQLPFHNFPLTCTDLATLTNILEHREAPIHLDF  
DGCPLPCHPCPEALVCGGQIENLSFKSRKCGDAFAEALSRSRLPTMGRLQMLG"
```

ORIGIN

```
1 gggagctctg agggagctctg cactatggaa acaacctgtc aatccagctc aaggcacaca  
61 tagcccagac acccatgaga ccctctccgt ggggacccta gagcacctat catgaacgag  
121 gagaccaagg ctggctcctc atggaccccg ttggcctcca gctcggcaac aagaacctgt  
181 ggagctgtct tgtgaggctg ctcaccaaag acccagaatg gctgaacgcc aagatgaagt  
241 tcttcctccc caacacggac ctggattcca ggaacgagac cttggaccct gaacagagag  
301 tcatcctgca actcaacaag ctgcatgtcc agggttcgga cacctggcag cttttcatte  
361 attgtgtgtg catgcagctg gaggtgcctc tggacctgga ggtgctgctg ctgagtactt  
421 ttggctatga tgatgggttc accagccagc tgggagctga ggggaaaagc caacctgaat  
481 ctcagctcca ccatggcctg aagcgcccac atcagagctg tgggtcctca ccccgccgga  
541 agcagtgcaa gaagcagcag ctagagttgg ccaagaagta cctgcagctc ctgcggacct  
601 ctgcccagca gcgctacagg agccaaatcc ctgggtcagg gcagcccccac gccttcacc  
661 aggtctatgt ccctccaatc ctgcgccggg ccacagcatc cttagacact ccggaggggg  
721 ccattatggg ggacgtcaag gtggaagatg gtgctgacgt gagcatctcg gacctcttca  
781 acaccagggt taacaagggc ccgagggtga ccgtgctttt ggggaaggct ggcattggga  
841 agaccacgct gggccaccgg ctctgccaga agtgggcaga gggccatctg aactgtttcc  
901 aggccctggt cctttttgaa ttccgccagc tcaacttgat cacgaggttc ctgacaccgt  
961 ccgagctcct ttttgatctg tacctgagcc ctgaatcgga ccacgacact gtcttcacgt  
1021 acctggagaa gaacgctgac caagtccctg tgatctttga tgggctagat gaggccctcc  
1081 agcctatggg tcctgatggc ccaggcccag tcctcaccct tttctcccat ctctgcaatg  
1141 ggacctcctt gcctggctgc cgggtgatgg ctacctcccg tccagggaag ctgcctgcct  
1201 gcctgcctgc agaggcagcc atgggtccaca tgttgggctt tgatgggcca cgggtggaag  
1261 aatatgtgaa tcaactcttc agcgcccagc catcgcgga gggggccctg gtggagttac  
1321 agacaaatgg acgtctccga agcctgtgtg cgggtgcccgc actgtgccaa gtgcctgtc  
1381 tctgcctcca ccatctgctt cctgaccag cccaggcca gtctgtggcc ctctgccc  
1441 acatgactca gctctatatg cagatggtgc tcgccctcag cccctctggg cacttgccc  
1501 cctcgccctt actggacctg ggggaggttg ccctgagggg cctggagaca gggaaggtta  
1561 tcttctatgc aaaagatatt gctccacctt tgatagcttt tggggccact cacagcctgc  
1621 tgacttcctt ctgcgtctgc acaggccctg ggcaccagca gacaggctat gctttcacc  
1681 acctcagcct gcaggagttt cttgctgccc tgcacctgat ggccagcccc aaggtgaaca  
1741 aagacacact taccagtat gttacctcc attcccgtg ggtacagcgg accaaagcta  
1801 gactgggcct ctcagaccac ctccccacct tcctggcggg cctggcatcc tgcacctgcc  
1861 gcccttctt tagccacctg gcgcagggca atgaggactg tgtgggtgcc aagcaggctg  
1921 ctgtagtga ggtgttgaa aagttggcca cccgcaagct cacagggcca aaggtttag  
1981 agctgtgtca ctgtgtggat gagacacagg agcctgagct ggccagtctc accgcacaaa  
2041 gcctccccta tcaactgccc ttccacaatt tcccactgac ctgcaccgac ctggccaccc  
2101 tgaccaacat cctagagcac agggaggccc ccatccacct ggattttgat ggctgtcccc  
2161 tggagcccca ctgccctgag gctctgtag gctgtgggca gatagagaat ctgagcttta  
2221 agagcaggaa gtgtggggat gcctttgcag aagccctctc caggagcttg ccgacaatgg  
2281 ggaggctgca gatgctgggg tgagccaggc cttggagctg agaagggtct tcagctgggg  
2341 atgcctggtt agcaggaagt aaaatcactg cccgaggcat cagccacctg gtgaaagctt  
2401 tgccctctctg tccacagctg aaagaagtca gttttcggga caaccagctc agtgaccagg  
2461 tgggtgctgaa cattgtggag gttctccctc acctaccag gctccggaag cttgacctga  
2521 gcagcaacag catctgcgtg tcaaccctac tctgcttggc aagggtggca gtcacgtgc
```



```
2581 ctaccgtcag gatgcttcag gccagggagg cggacctcat cttcctttctt tccccgcca
2641 ccgagacaac tgcagagcta caaagagctc cagacctgca ggaaagtgac ggccagagga
2701 aaggggctca gagcagaagc ttgacgctca ggctgcagaa gtgtcagctc caggctccacg
2761 atgcggaggc cctcatagcc ctgctccagg aaggccctca cctggaggaa gtggaaggag
2821 gaagttaagc tgcagaaaga taaacttgct caaggccaca caggtaggaa gagtctaggc
2881 tagggttcaa gccagacag tctggctcgc agcctcatcc tcataaccac tgctacctct
2941 cttgctgaga tctgccaagt agaaaccca ccacacctgg gtctgccttc caaacacag
3001 tccctcaggg ctccccccac ccccttcac cttctcccag agtagagtgg gataaccttc
3061 tcttttcggg atggagatat tcccatggcg tccagcccct ggctgaagcc aataagagta
3121 gtgcttgggg atggacggag gctctgtcac gacctagga ggggcgcccc tccaggaaac
3181 ctccaagtga acatgaaggc agatgatgga acgccaggat gtgttctggg tcgagtggcc
3241 ccacctcagg cctctcaggg aaccagctgg aagatgaagg ctgtcggctg atggcagagg
3301 ctgcatccca gctgcacatc gccaggaagc tggacctcag cgacaacggg ctttctgtgg
3361 ccggggtgca ttgtgtgctg agggcgtgta gtgcgtgctg gacctggca gagctgcaca
3421 tcagcctgca gcacaaaact gtgatcttca tgtttgcca ggagccagag gagcagaagg
3481 ggccccagga gagggtgca tttcttgaca gcctcatgct ccagatgccc tctgagctgc
3541 ctctgagctc ccgaaggatg aggtgacac attgtggcct ccaagaaaag cacctagagc
3601 agctctgcaa ggctctggga ggaagctgcc acctcggta cctccacctc gacttctcag
3661 gcaatgctct gggggatgaa ggtgcagccc ggctggctca gctgctccca gggctgggag
3721 ctctgcagtc cttgaacctc agtgagaacg gtttgcctt ggatgccgtg ttgggtttgg
3781 ttcggtgctt ctccactctg cagtggctct tccgcttggg catcagcttt gaaagccaac
3841 acatcctcct gagaggggac aagacaagca gggatatgtg ggccactgga tctttgccag
3901 acttcccagc tgcagccaag ttcttagggg tccgtcagcg ctgcatcccc aggagcctct
3961 gcctcagtga gtgtcctctg gagcccccaa gcctcaccgg cctctgtgcc actctgaagg
4021 actgcccggg acccctggaa ctgcaccctg ccccatgaga gtccccctggc ctttggtaga
4081 aacttggctg tctctcggca gccccagcc ttaggcagcg catgtctccc actgggagat
4141 gctgtgctgg actggggaag ccttcacctg caccatccac tcaactcagg gcacctggga
4201 gccctgtcca cctccaacct caccctgga gcctcaccag ggcacccact tgaacctgcc
4261 tgcattggctg gagcgtagca cttctgaaag cccttcctca aggcaccccc actctccttg
4321 gggttaccac ctactcgc ccagaacatc tgggtctgta accagagact ggacctggaa
4381 tcaggactct tggctcaaaa gggatttaac tccccgggc tcagcttctt catctgcaca
4441 gtggatggct agcctttcct tttattgtca ttgtggtgat tctattatag taattacctt
4501 aaaataaaga aatccaagac
```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42



EGCTCAGGATACAGACTTCTGCTAGAGATCGGATCCCGGGGCTATTATATAGCTCGATCGATCT
TTCTCTTATATCTGCGCTATGCGCTATATACACACACATCGCGGATAGCATGACTGATCTA
CCCATCT
CACAGACT

Nucleotide

My NCBI
[\[Sign In\]](#)
[\[Register\]](#)

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Limits Preview/Index History Clipboard Details

Display ☒ Show ☒ Send to ☒

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [AK090431](#). Reports Homo sapiens mRNA...[gi:21748549]

[Links](#)

LOCUS AK090431 6604 bp mRNA linear PRI 15-JUL-2002

DEFINITION Homo sapiens mRNA for FLJ00348 protein.

ACCESSION AK090431

VERSION AK090431.1 GI:21748549

KEYWORDS fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1

AUTHORS Jikuya,H., Takano,J., Kikuno,R., Nagase,T. and Ohara,O.

TITLE The nucleotide sequence of a long cDNA clone isolated from human spleen

JOURNAL Published Only in Database (2002)

REFERENCE 2 (bases 1 to 6604)

AUTHORS Jikuya,H., Takano,J., Kikuno,R., Nagase,T. and Ohara,O.

TITLE Direct Submission

JOURNAL Submitted (04-JUL-2002) Takahiro Nagase, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/NEDO, Tel:81-438-52-3913, Fax:81-438-52-3914)

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert and 5'- & 3'-end one pass sequencing: Research Association for Biotechnology; cDNA library construction and clone selection: Kazusa DNA Research Institute.

FEATURES Location/Qualifiers

source 1..6604
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="FLJ00348"
/tissue_type="spleen"
/dev_stage="adult"
/note="vector:pBluescriptII SK plus"

gene 1..6604
/gene="FLJ00348"

CDS <431..2767
/gene="FLJ00348"
/inference="non-experimental evidence, no additional details recorded"
/note="Start codon is not identified."
/codon_start=1

```
/product="FLJ00348 protein"  
/protein_id="BAC03412.1"  
/db_xref="GI:21748550"  
/translation="LSLPSVTYLLLEVIPDSMRKQEVRTGREAGQGHGTGSPAQVKA  
LMDLLAGKGSQGSQAPQALDRTDPAPLGPSCNDSRIQRHRKALLSKVGGGPELGPPWH  
RLASLLLVEGLTDLQLEHDFTEATRGGGHPARTVALDRLFLPLSRVSVPPRVSIT  
IGVAGMGKTTLVRHFVRLWAHQVVGKDFSLVPLTFRDLNTHKLCADRLICSVFPHV  
GEPSLAVAVPARALLILDGLDECRTPLDFSNTVACTDPKKEIPVDHLITNIIRGNLFP  
EVSIIWITSRPSASGQIPGGLVDRMTEIRGFNEEEIKVCLEQMFPEQALLGWMLSQVQ  
ADRALYLMCTVPAFCRLTGMAIGHLWRSRTGPDDELWPPRTLCELYSWYFRMALS  
GQEKGPASPRIEQVAHGGRKMVGTGLRLAFHGLLKKKYVFYEQDMKAFGVLDLALLQGA  
PCSCFLQREETLASSVAYCFTHLSLQEFVAAAYYGGASRRRAIFDLFTESGVSWPRLGF  
LTHFRSAAQRAMQAEDGRDLVFLRFLSGLSPRVNALLAGSLLAQGEHQAYRTQVAEL  
LQGCRLPDAAVCARAINVLHCLHELQHTELARSVEEAMESGALARLTGPAHRAALAYL  
LQVSDACAQEANLSLSLQGVLSQLLPQLLYCRKLRLDTNQFQDFVMELLSVLSGKD  
CRIQKISLAENQISNKGAKALARSLLVNRSLSLTLDRGNSIGPQAKALADALKINRT  
LTSLRVKFMYHKIDCFRRVPEADACNPSTLGGQGRWIT"
```

ORIGIN

```
1 gccacagggga cagccggtgg gctcggtggg gctgcagaag gtcagggctg cactgctctc  
61 ggccccacaca cggttggttg gttggcggtg taagtgcctt gatccctggt cctgagaact  
121 caggctggca cagggattcc cagggcatct accaccacgc agctggagca gggctgagcc  
181 caggagcatg gagatggacg cccccaggcc cccagtcctt gctgtccctg gagcagcatc  
241 gaggcccgga agggctgcca tcagcagcag tgagccatca cctctgctgg ccacattgtg  
301 ttttttctcc tagaactgtg gacaacggaa ggctgagccc catccattga gttcctgggg  
361 cccactgga ggggctgctg tggccagggt gcacggtcac aaatgaagac accaaggcgc  
421 agagaggtga ctcagcctgc cctcagtcac ctatctgctc ctggaggtga tccccgactc  
481 catgaggaag caagaggtgc ggacgggcag ggaggccggc cagggccacg gtacgggctc  
541 cccagccgag caggtgaaag ccctcatgga tctgctgggt gggaaggcca gtcaaggctc  
601 ccaggccccg caggccctgg ataggacacc ggatgccccg ctggggccct gcagcaatga  
661 ctcaaggata cagaggcacc gcaaggccct gctgagcaag gtgggaggtg gcccgagct  
721 gggcggaacc tggcacaggc tggcctccct cctgctgggt gagggcctga cggacctgca  
781 gctgagggaa cagacttca cacaggtgga ggccaccgcg gggggcgggc accccgccag  
841 gaccgtcgcc ctggaccggc tcttctctgc tctctcccg gtgtctgtcc caccgccggg  
901 ctccatcact atcggggtgg ccggcatggg caagaccacc ctggtgagga acttcgtccg  
961 cctctgggcc catgggcagg tcggcaagga cttctcgctg gtgctgcctc tgacctccg  
1021 ggatctcaac acccacgaga agctgtgtgc cgaccgactc atctgctcgg tcttcccgca  
1081 cgtcggggag cccagcctgg cggtggcagt cccagccagg gccctcctga tcttggaagg  
1141 cttggatgag tgcaggacgc ccttgagact ctccaacacc gtggcctgca cggacccaaa  
1201 gaaggagatc ccggtggacc acctgatcac caacatcac cgtggcaacc tcttcccgga  
1261 agtttccatc tggatcacct cccgtcccag tgcattctggc cagatccag ggggctgggt  
1321 ggaccggatg acggagatcc ggggctttaa cgaggaggag atcaagggtg gtttgagca  
1381 gatgttcccc gaggaccagg cccttctggg ctggatgctg agccaagtgc aggtgacag  
1441 ggccctgtac ctgatgtgca ccgtcccagc cttctgcagg ctcacgggga tggcgctagg  
1501 ccacctgtgg cgcagcagga cggggcccca ggatgcagag ctgtggcccc cgaggacct  
1561 gtgcgagctc tactcatggt actttaggat ggccctcagc ggggaggggc aggagaaggg  
1621 caaggcaagc cctcgcatcg agcaggtggc ccatggtggc cgcaagatgg tggggacatt  
1681 gggccgtctg gccttccatg ggctgctcaa gaagaaatac gtgttttacg agcaagacat  
1741 gaaggcgttt ggtgtagacc tcgctctgct gcaggcgcc cgtgcagct gcttctgca  
1801 gagagaggag acgttgatg cgtcagtggt ctactgctc accacctgt ccctgcagga  
1861 gtttggtggca gccgcgtatt actatggcgc atccaggagg gccatcttcg acctcttcac  
1921 tgagagcggc gtatcctggc ccaggctggg cttcctcacg catttcagga gcgcagccca  
1981 gcgggcccag caggcagagg acgggagggt ggacgtgttc ctgcgcttc tctccggcct  
2041 cttgtctccg agggatcaat ccctcctggc cggctccctg ctggcccaag gcgagacca  
2101 ggccatccgg acccaggtgg ctgagctcct gcagggtgc ctgcgcccc atgccgcagt  
2161 ctgtgcacgg gccatcaacg tgttgactg cctgcatgag ctgcagcaca ccgagctggc  
2221 ccgcagcgtg gaggaggcca tggagagcgg ggccctggcc aggtgaccg gtcccgcgca  
2281 ccgcgctgcc ctacgctacc tctgaggtg gtccgacgc tgtgcccagg aggccaacct  
2341 gtccttgagc ctcagccagg gcgtccttca gagcctgctg cccagctgc tctactgccg  
2401 gaagctcagg ctggacacca accagttcca ggaccccggt atggagctgc tgggcagcgt  
2461 gctgagtggt aaggactgtc gcattcagaa gatcagcttg gcggagaacc agatcagtaa
```

2521 caaagggggcc aaagctctgg ccagatccct cttgggtcaac agaagtctga cctctctgga
2581 cctccgcgggt aactccattg gaccacaagg ggccaaggcg ctggcagacg ctttgaagat
2641 caaccgcacc ctgacctccc tgagggtgaa attcatgtac cataaaattg actgttttag
2701 gcgggtccca gaggtgatg cctgtaatcc cagcactttg ggaggccaag ggaggtggat
2761 cacttgaggt cgggagttcg agaccagcct ggccaacatg cctccagggc aacaccgtta
2821 gggatgatgg tgccagggtcc atggctgagg ccttggcctc caaccggacc ctctccatgc
2881 tgcacctgca gaagaacagc atcggggcca tgggagccca gcggatggca gatgcctcga
2941 agcagaacag gagtctgaaa gagctcatgt tctccagtaa tagtatcggg gatggaggtg
3001 ccaaggccct ggctgaggcc ctgaagggtga accagggcct ggagagcctg gacctgcaga
3061 gcaattccat cagtgcgca ggagtggcag cactgatggg ggccctctgc accaaccaga
3121 acctcctcag cctcagcctt cgagaaaact ccatacgtcc cgagggagcc caggccatcg
3181 gtcatgccct ctgcgccaac agcaccctga agaacctgga cctgacagcc aacctcctcc
3241 acgaccaggg tgcccggggc atcgcagtgg cagtgcgaga aaaccgcacc ctccactccc
3301 ttcacctgca gtggaacttc atccaggccg gcgctgccc aagccctggga caagcactac
3361 agctcaacag gagcctcacc agcttagatt tacaggagaa cgccatcggg gatgcaggag
3421 cgtgtgcggg ggcccgtgca ctgaagggtca acacagccct cactgctctc tatctccagg
3481 tggcctcaat tgggtgcttca ggcgcccagg tgctagggga agccttggct gtgaacagaa
3541 ccttggagat tctcgactta agaggaaatg ccattggggg ggctggagcc aaagcccctg
3601 gccaaatgct ctgaaggtaa actcaagtct ccggagactc aatcttcaag agaattctct
3661 ggggatggac ggggcgatat gcattgccac agcactgtct ggaaaccaca ggctccagca
3721 tatcaatctc cagggaacc acattgggga ctccggggcc aggatgatct cagaggccat
3781 caagacaaat gctcccacgt gcactgttga aatgtgatcc tggtaggacg atcaggagaa
3841 tgggcagatg ctgagctgga agcttttgaa cagaaaggcc gacttctggg gggcctgtct
3901 gggagctggg aacgctgctt gctcagcacg agagccgggc tctgcaggga ggaaggagag
3961 gtgctgccgg aggaggtcgt gagctcctct tctgctgcag gagtgggtcca ggcagggggg
4021 gacgggtact ctgttatggc acagagaagg gaggggccac cccaaggga ctaggggcca
4081 aaggcctgaa agctgagcag tacaggaggc tggttccagc tttacaccct gaggacttca
4141 tgtgtcccca accttataaa atgtttatta ctgccccttt cactcacct ggtaaaaaat
4201 catcccatgc tctgagatga gctgccacct caagcccgtg aggagcatcc gtttggtagg
4261 ggtaacagag gggacccttc tttatcttct caagaagaag atttcagggt atcatcctta
4321 cagacatgaa aaagctatgg gaaaattgtg aagataaatg aaagttttaa ttctaggatt
4381 ctggaaacag agacagtaag agttctccaa ggattttgccc ttttttgggt gtttttgaga
4441 tggagtctcg ctcttgtcgc ccaggctgga gtgcagtggc acgatctcag ctccctgcaa
4501 cctccgcctc ccgggttcac gtgattctcc tgcctcagcc tccccagtag ctgggaatac
4561 aggcacccgc caccatgccc ggctaatttt ttagatttta gttagagcgg ggtttcatca
4621 tgttgccag gctgggtctcg aactcctgac ctgaggtgat ccatacagct gggcctccca
4681 aagtactggg attacaggca tgagccacca cacctggccc cattttttat ttattacaaa
4741 atcaaagaca tgggtgatgc ctggcacatg ttgtctggag tctggcacac tggttatcaa
4801 tagcacattc agtgtattca gtgatgtcat tctttattta tttttgagac agaattctgtc
4861 acccaggctg gagtgcagtg gcatgatctc agctcactgt aggtcttacc tcatgggttc
4921 cagtgattct cctgcctcgg cctcccaagt agttgggtct acaggcacgc accaccacac
4981 ccagctaatt tttgtatttt tagtagagat ggggtttcac catgttgatc aggtggtct
5041 tgaactcctg acctcaagt atccaccac ctgagcctcc caaagtgtg ggattacagg
5101 tgtgagccac tgcacctggc agtgatgtca ttccttacta ggcttccaaa gccactgctg
5161 tggccacagc ttccatggag acaggcaagc tgagcctcta tgtggacca attcctgcag
5221 ctgttttgtg tggaggga aaatccaaa tggacatcaa cagctttcat caactaaata
5281 accacagaaa atatttatga agactataaa gcaatgatta cttttgaatt ggaaaggat
5341 cactattatt tgaaatgttt cttcaaaagt gagcatccgg acaggaacca tcatggatgc
5401 tgaggccatg gatgaaggcc tactcgggaa gatgatatcc ttgcagtctc aaaacggcac
5461 cccacaaagg tgatatccta atttacaag ggaaaaagg accttaatct gaaatctggc
5521 aaatgcagcc tcaacagaag tgacagaatt gaacatcgcc aataatggga cacacagaca
5581 tcacatgccc ccagtctgat gcaccacgga gtcgtctctg atgtattctt gtcaaaaaat
5641 gtttgccctga ttctaatacat gaaagaacaa ttagaaaaaa tccaaattga cagatattct
5701 gcagaataaa tggcctgacc tcatcaaaaa catcaatgtc atgaaaaaca caaaacattg
5761 cagatagcgt gaaattaaag attacagaga tataacttaa tgcaagatct ctgactggat
5821 cctagactgc aggaaaaagt ctgctataaa gaacatttgg atcacttgta gtagctggga
5881 aataaaacaa aacattattt gtaaaagggg ggaatctga acatgggtct tgcagtatct
5941 atgacagttt ttgcggggca gagatttcta gattgacagc tgttttagta ctttcaaggt
6001 gatgctctgt ctgctgggtt gcattgtttc tgtctgagtt aagagactgg cagaacacag
6061 agttgcagta gccaaacact ggagaaagct gggccctaca gaaacctaac gctgaagaaa

```
6121 cctcaggagc caaactggtg gagaaaacaa agagtccctc ctctctccct tttcaaataa
6181 tgatcataca tcttcaagct gtctgaaatg gttaaggagt tcagtctgtc gtcaggcaca
6241 caccagagcc agctagccca cacagacccc atcagagcaa aacagacaag agaatttaat
6301 tcatatccac atagaaagga cttctaggta ggaggtagac ccttttagctc cttccaatt
6361 aaaggagtcc ccaattctgg cacctgagag tcccctgggt ctaacagcta tgatatttat
6421 gtagtgtgtt gcttacctaa atgaatacaa tttccttcca gacacgtgac actgatatta
6481 aagtgcta at gagagggatc tattttcttct tgtacgctaa aagagaaaaca gcagttcaga
6541 tttcccatca gaagtccgag gactttgttc ttgataacta ctaccaataa aaattgagta
6601 tttg
```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42




[\[Sign In\]](#)
[\[Register\]](#)

[PubMed](#)
[Nucleotide](#)
[Protein](#)
[Genome](#)
[Structure](#)
[PMC](#)
[Taxonomy](#)
[OMIM](#)
[Books](#)

Search for

Limits Preview/Index History Clipboard Details

Display **GenBank** Show **5** Send to

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

1: [AK090439](#). Reports Homo sapiens mRNA...[gi:21748565]

Links

LOCUS AK090439 5833 bp mRNA linear PRI 15-JUL-2002

DEFINITION Homo sapiens mRNA for FLJ00359 protein.

ACCESSION AK090439

VERSION AK090439.1 GI:21748565

KEYWORDS fis (full insert sequence).

SOURCE	Homo sapiens (human)
--------	----------------------

ORGANISM	Homo sapiens
----------	--------------

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE	1
-----------	---

AUTHORS Jikuya, H., Takano, J., Kikuno, R., Nagase, T. and Ohara, O.

TITLE The nucleotide sequence of a long cDNA clone isolated from human spleen

JOURNAL Published Only in Database (2002)

REFERENCE 2 (bases 1 to 5833)

AUTHORS Jikuya, H., Takano, J., Kikuno, R., Nagase, T. and Ohara, O.

TITLE Direct Submission

JOURNAL Submitted (04-JUL-2002) Takahiro Nagase, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/NEDO, Tel:81-438-52-3913, Fax:81-438-52-3914)

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert and 5'- & 3'-end one pass sequencing: Research Association for Biotechnology; cDNA library construction and clone selection: Kazusa DNA Research Institute.

FEATURES	Location/Qualifiers
----------	---------------------

```

source      1.5833
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="FLJ00359"
            /tissue_type="spleen"
            /dev_stage="adult"
            /note="vector:pBluescriptII SK plus"

```

gene 1..5833
/gene="FLJ00359"

```
CDS
<1..3172
/gene="FLJ00359"
/inference="non-experimental evidence, no additional
details recorded"
/note="Start codon is not identified."
/codon start=2
```

/product="FLJ00359 protein"
/protein_id="BAC03420.1"
/db_xref="GI:21748566"
/translation="SELLFDLYLSPESDHDTVFQYLEKNADQVLLIFDGLDEALQPMG
PDGPGPVLTLFSLCNGTLLPGCRVMATSRPGKLPACLPAAEAMVHMLGFDGPRVEEY
VNHFFSAQPSREGALVELQTNGRLRSLCAVPALCQVACLCLHLLPDHAPGQSVALLP
NMTQLYMQMVLALSPPGHLLTSSLLDLGEVALRGLETGKVIIFYAKDIAPPLIAFGATH
SLLTSFCVRTGPGHQQTGYAFTHLSLQEFLLAALHLMASPKVNKDTLTQYVTLHSRWVQ
RTKARLGLSDHLPTFLAGLASCTCRPFLSHLAQGNEDCVGAKQAAVVQVLKKLATRKL
TGPKVVELCHCVDETQEPELASLTAQSLPYQLPFHNFPLTCTDLATLTNILEHREAPI
HLDFDGCPLPHCPEALVCGGQIENLSFKSRKCGDAFAEALSRLPTMGRLQMLGLAG
SKITARGISHLVKALPLCPQLKEVSFRDNQLSDQVVLNIVEVLPHLPRLRKLDSLSSNS
ICVSTLLCLARVAVTCPTVRMLQAREADLIFLLSPPTETTAELQRAPDLQESDGQRKG
AQSRSLTLRLQKCQLQVHDAEALIALLOEGPHLEEVDSLGNQLEDEGCRLMAEASQL
HIARKLDLSDNGLSVAGVHCVLRVAVSACWTLAELHISLQHKTVIFMFAQEPEEQKGPG
ERAAFLDSLMLQMPSELPLSSRRMRLTHCGLQEKHLEQLCKALGGSCHLHLLHLDLFD
NALGDEGAARLAQLLPGLGALQSLNLSENGLSLDAVLGLVRCFSTLQWLFRDLISFES
QHILLRGDKTSRDMWATGSLPDFPAAAKFLGFRQRCIPRSLCLSECPLEPPSLTRLCA
TLKDCPGPLELQLSCEFLSDQSLETLLDCLPQLPQLSLLQLSQTGLSPKSPFLLANTL
SLCPRVKVDLRLSLHATLHFRSNEEEEGVCCGRFTGCSLSQEHVESLCWLLSKCKDL
SQVDLSANLLGDSGLRCLLECLPQVPISGLLDLSHNSISQESALYLLETLPSCPRVRE
ASVKCLGSWHVWAPCFPRPFSLQPGI"

ORIGIN

```
1  gtccgagctc  ctttttgcac  tgtacctgag  ccctgaatcg  gaccacgaca  ctgtcttcca
61  gtacctggag  aagaacgctg  accaagtcct  gctgatcttt  gatgggctag  atgaggccct
121 ccagcctatg  ggtcctgatg  gcccaggccc  agtcctcacc  cttttctccc  atctctgcaa
181 tgggaccctc  ctgcctggct  gccgggtgat  ggctacctcc  cgtccaggga  agctgcctgc
241 ctgcctgcct  gcagaggcag  ccatgggtcca  catgttgggc  tttgatgggc  cacgggtgga
301 agaatatgtg  aatcacttct  tcagcgccca  gccatcgcg  gagggggccc  tgggtggagt
361 acagacaaat  ggacgtctcc  gaagcctgtg  tgcggtgccc  gcactgtgcc  aagtcgcctg
421 tctctgcctc  caccatctgc  ttctgacca  cgccccagge  cagtctgtgg  ccctcctgcc
481 caacatgact  cagctctata  tgcagatggg  gctcgccctc  agccccctg  ggcacttgct
541 cacctcgctc  ctactggacc  tgggggaggt  ggccctgagg  ggccctggaga  cagggaaggt
601 tatcttctat  gcaaaagata  ttgctccacc  cttgatagct  tttggggcca  ctcacagcct
661 gctgacctcc  ttctgcgtcc  gcacaggccc  tgggcaccag  cagacaggct  atgctttcac
721 ccacctcagc  ctgcaggagt  ttcttgctgc  cctgcacctg  atggccagcc  ccaaggtgaa
781 caaagacaca  cttaccagat  atgttaccct  ccattcccgc  tgggtacagc  ggaccaaaagc
841 tagatggggc  ctctcagacc  acctccccc  cttcctggcg  ggcctggcat  cctgcacctg
901 ccgccccctc  cttagccacc  tggcgcaggg  caatgaggac  tgtgtgggtg  ccaagcaggc
961 tgctgtagtg  cagggtgttg  agaagttggc  caccgcgaag  ctcacagggc  caaaggttgt
1021 agagctgtgt  cactgtgtgg  atgagacaca  ggagcctgag  ctggccagtc  tcaccgcaca
1081 aagcctcccc  tatcaactgc  ccttcacaca  tttcccaactg  acctgcaccg  acctggccac
1141 cctgaccaac  atcctagagc  acaggggaggc  ccccatccac  ctggattttg  atggctgtcc
1201 cctggagccc  cactgccctg  aggctctggt  aggctgtggg  cagatagaga  atctcagctt
1261 taagagcagg  aagtgtgggg  atgcctttgc  agaagccctc  tccaggagct  tggcgacaat
1321 ggggaggctg  cagatgctgg  ggttagcagg  aagtaaaatc  actgcccag  gcatcagcca
1381 cctggtgaaa  gctttgcctc  tctgtccaca  gctgaaagaa  gtcagttttc  gggacaacca
1441 gctcagtgac  caggtggtgc  tgaacattgt  ggaggttctc  cctcacctac  cacggctccg
1501 gaagcttgac  ctgagcagca  acagcatctg  cgtgtcaacc  ctactctgct  tggcaagggt
1561 ggcagtcacg  tgtcctaccg  tcaggatgct  tcaggccagg  gaggcggacc  tcatcttcct
1621 tctttccccc  cccacagaga  caactgcaga  gctacaaaga  gctccagacc  tgcaggaaag
1681 tgacggccag  aggaaagggg  ctcagagcag  aagcttgacg  ctcaggctgc  agaagtgtca
1741 gctccaggtc  catgatgcgg  aggccctcat  agccctgctc  cagggaaggc  ctcacctgga
1801 ggaagtggac  ctctcaggga  accagctgga  agatgaaggc  tgtcggctga  tggcagaggc
1861 tgcaccccag  ctgcacatcg  ccaggaaagt  ggacctcagc  gacaacgggc  tttctgtggc
1921 cggggtgcat  tgtgtgctga  gggccgtgag  tgcgtgctgg  accctggcag  agctgcacat
1981 cagcctgcag  cacaaaactg  tgatcttcat  gtttgcccag  gagccagagg  agcagaaggg
2041 gccccaggag  agggctgcag  ttcttgacag  cctcatgctc  cagatgccct  ctgagctgcc
2101 tctgagctcc  cgaaggatga  ggctgcacac  ctgtggcctc  caagaaaagc  acctagagca
2161 gctctgcaag  gctctgggag  gaagctgcca  cctcggtcac  ctccacctcg  acttctcagg
```

```

2221 caatgctctg ggggatgaag gtgcagcccg gctggctcag ctgctcccag ggctgggagc
2281 tctgcagtc ttgaacctca gtgagaacgg tttgtccctg gatgccgtgt tgggtttggt
2341 tcggtgcttc tccactctgc agtggctctt ccgcttgga acagctttg aaagccaaca
2401 catcctcctg agaggggaca agacaagcag ggatatgtgg gccactggat ctttgccaga
2461 cttcccagct gcagccaagt tcttaggggt ccgtcagcgc tgcacccca ggagcctctg
2521 cctcagtgag tgtcctctgg agccccaag cctcaccgc ctctgtgcca ctctgaagga
2581 ctgcccggga cccctggaac tgcaattgtc ctgtgagttc ctgagtgacc agagcctgga
2641 gactctactg gactgcttac ctcaactccc tcagctgagc ctgctgcagc tgagccagac
2701 gggactgtcc ccgaaaagcc ccttcctgct ggccaacacc ttaagcctgt gtccacgggt
2761 taaaaaggtg gatctcaggt ccctgcacca tgcaactttg cacttcagat ccaacgagga
2821 ggaggaaggc gtgtgctgtg gcaggttcac aggtgcagc ctcagccagg agcacgtaga
2881 gtcactctgc tggttgctga gcaagtgtaa agacctcagc caggtggacc tctcagcaaa
2941 cctgctgggc gacagcggac tcagatgcct tctggaatgt ctgccgagg tgcccctctc
3001 cggtttgctt gatctgagtc acaacagcat ttctcaggaa agtgccctgt acctgctgga
3061 gacactgccc tcctgcccac gtgtccggga ggctcagtg aagtgcctag gaagctggca
3121 tgtctgggca ccgtgcttcc ccaggccctt ctctctgcag cctgggctct gagcagagct
3181 tccggattca tttctccaga gaggaccagg ctgggaagac actcaggcta agtgagtga
3241 gcttccggcc agagcacgtg tccaggctgg ccaccggctt gagcaagtcc ctgcagctga
3301 cggagctcac gctgaccag tgctgcctgg gccagaagca gctggccatc ctctgagct
3361 tgggtggggc acccgcagg ctgttcagcc tcagggtgca ggagccgtgg gcggacagag
3421 ccagggttct ctccctgtta gaagtctgcg ccaggcctc aggagtgct actgaaatca
3481 gcatctccga gaccagcag cagctctgtg tccagctgga atttctctgc caggaagaga
3541 atccagaagc tgtggcactc aggttggtct actgtgacct tggagcccac cacagccttc
3601 ttgccgggca gctgatggag acatgtgcca ggctgcggca gctcagcttg tctcaggtta
3661 acctctgtga ggacgatgat gccagttccc tgtctgtgca gagcctcctg ctgtccctct
3721 ctgagctgaa gacatttcgg ctgacctcca gctgtgtgag caccgagggc ctgcccacc
3781 tggcatctgg tctgggccac tgccaccact tggaggagct ggacttgtct aacaatcaat
3841 ttgatgagga gggcaccaag gcgctgatga gggcccttga ggggaaatgg atgctaaaga
3901 ggctggacct cagtcacctt ctgctgaaca gctccacctt ggccttgctt actcacagac
3961 taagccagat gacctgcctg cagagcctca gactgaacag gaacagtatc ggtgatgtcg
4021 gttgctgcca ctttctgag gctctcagg ctgccaccag cctagaggag ctggacttga
4081 gccacaacca gattggagat gctggtgtcc agcacttagc taccatcctg cctgggctgc
4141 cagagctcag gaagatagac ctctcaggga atagcatcag ctgagccggg ggagtgcagt
4201 tggcagagtc tctcgttctt tgcaggcgcc tggaggagtt gatgcttggc tgcaatgccc
4261 tgggggatcc cacagccctg gggctggctc aggagctgcc ccagcacctg agggctctac
4321 acctaccatt cagccatctg ggcccagggt gggccctgag cctggcccag gccctggatg
4381 gatcccccca tttggaagag atcagcttgg cggaaaacaa cctggctgga ggggtcctgc
4441 ttttctgtat ggagctcccg ctgctcagac agatagacct ggtttcctgt aagattgaca
4501 accagactgc caagctcctc acctccagct tcacgagctg ccctgccctg gaagtaatct
4561 tgctgtcctg gaatctcctc ggggatgagg cagctgccga gctggcccag gctgtgcgc
4621 agatgggccc gctgaagaga gtggacctgg agaagaatca gatcacagct ttggtggcct
4681 ggctcctggc tgaaggactg gcccaggggt ctagcatcca agtcatccgc ctctggaata
4741 accccattcc ctgcgacatg gcccagcacc tgaagagcca ggagcccagg ctggactttg
4801 ctttctttga caaccagccc cagggccctt tggggtactt gatggcccc tcaagacctt
4861 tggaatccag ccaagtgatg caccctaatg atccacctt cgcccactgg gataaatgac
4921 tcaggaaaga agagcctcgg cagggcgctc tgcactccac ccaggaggaa ggatacgtgt
4981 gtctgtctgc agtcctcagg gagaactttt ttgggaacca ggagctgggt ctggacaaag
5041 gagtaccctg cattacgtgg gatattgtgt atcaattggg gacatgcgac acacaatgag
5101 ggtgtcatga caatgcatga cacgtacggt tatatgtggc agtgtgacct cttgacatgt
5161 ggcgttacat gaaagtcagt gtggcacgtg ttctgtggca tgggtgctgg catcccaagt
5221 ggcaggatac atgattgttg gtctatatat gacacatgac aaatgtccat gtcacaggac
5281 tcatggctgg ccagatgacc tcaggctggc ccaagatcta atttattaat ttttaaagca
5341 aatacatatt tatagattgt gtgtatggag cagctaagtc agggaaaagtc ttccgccga
5401 gctgggaggg gagagtgtcc atgcaactgac cagtccaggg gctcaagggc cagggctctg
5461 gaacaagcca gggactcagc cattaagtcc cctcctgct caatcctcag cctaccatc
5521 tataaacttg atgactcctc cttacttac atactagctt ccaaggacag gtggaggtag
5581 ggccagcctg gcgggagtgg agaagcccag tctgtcctat gtaagggaca aagccaggtc
5641 taatggtact gggtaggggg cactgccaag acaataagct aggtactagg gtccagctac
5701 tactttggtg ggattcaggt gagtctccat gcacttcaca tgttaccag tgttcttgtt
5761 acttccaagg agaaccaaga atggctctgt cacactcgaa gccaggtttg atcaataaac




```


5821 acaatggtat tcc

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)


Oct 4 2005 13:52:42




[\[Sign In\]](#)
[\[Register\]](#)

PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	OMIM	Books
--------	------------	---------	--------	-----------	-----	----------	------	-------

Search

Limits Preview/Index History Clipboard Details

Display **GenBank**  Show **5**  Send to 

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [AK090476](#). Reports Homo sapiens mRNA...[gi:21748639]

Links

LOCUS	AK090476	4191 bp	mRNA	linear	PRI 15-JUL-2002
-------	----------	---------	------	--------	-----------------

DEFINITION Homo sapiens mRNA for FLJ00398 protein.

ACCESSION AK090476

VERSION AK090476.1 GI:21748639

KEYWORDS **fis** (full insert sequence).

SOURCE . Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1

AUTHORS Jikuya, H., Takano, J., Kikuno, R., Nagase, T. and Ohara, O.

TITLE The nucleotide sequence of a long cDNA clone isolated from human spleen

JOURNAL Published Only in Database (2002)

REFERENCE 2 (bases 1 to 4191)

AUTHORS Jikuya, H., Takano, J., Kikuno, R., Nagase, T. and Ohara, O.

TITLE Direct Submission

JOURNAL Submitted (04-JUL-2002) Takahiro Nagase, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:<http://www.kazusa.or.jp/NEDO>, Tel:81-438-52-3913, Fax:81-438-52-3914)

COMMENT	NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert and 5'- & 3'-end one pass sequencing: Research Association for Biotechnology; cDNA library construction and clone selection: Kazusa DNA Research Institute.
---------	--

FEATURES	Location/Qualifiers
----------	---------------------

```
source      1..4191
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="FLJ00398"
            /tissue_type="spleen"
            /dev_stage="adult"
            /note="vector:pBluescriptII SK plus"
```

gene 1..4191
/gene="FLJ00398"

```
CDS
    /gene="FLJ00398"
    <374..2356
    /gene="FLJ00398"
    /inference="non-experimental evidence, no additional
    details recorded"
    /note="Start codon is not identified."
    /codon start=1
```

```
/product="FLJ00398 protein"  
/protein_id="BAC03457.1"  
/db_xref="GI:21748640"  
/translation="LSLPSVTYLLLEVIPDSMRKQEVRTGREAGQGHGTGSPAQVKA  
LMDLLAGKGSQGSHPQALDRTPDAPLGPCSNDSRIQRHRKALLSKVEATRGGGHPAR  
TVALDRLFLPLSRVSVPPRVSITIGVAGMGKTTLVRFVRLWAHGQVGKDFSLVLPLT  
FRDLNTHEKLCADRLICSVFPHVGEPSLAVAVPARALLILDGLDECRTPLDFSNTVAC  
TDPKKEIPVDHLITNIIRGNLFPEVSIWITSRPSASGQIPGGVLDRMTEIRGFNEEEI  
KVCLEQMFPEQDALLGWMLSQVQADRALYLMCTVPAFCRLTGMAHGHLWRSRTGPQDA  
ELWPPRTLCELYSWYFRMALSGEGQEKGPRIEQVAHGGRKMVGTLGRALFHGLLK  
KKYVFYEQDMKAFGVLDLALLQGAPCSCFLQREETLASSVAYCFTHLSLQEFVAAAYY  
GASRRATFDLFTESGVSWPRLGFLTHFRSAAQRAMQAEGRDLVFLRFLSGLLSPRVN  
ALLAGSLLAQGEHQAYRTQVAELLQGCRLPDAAVCARAINVLHCLHELOHTELARSVE  
EAMESGALARLTGPAHRAALAYLLQVSDACAQAEANLSLSLSQGVLSLLPQLLYCRKL  
RWIPGQGAGAGEGAEEAEAVPSPPPSFSVSLGLLP"
```

ORIGIN

```
1 cggagccaca gggacagccg gtgggctcgg tggggctgca gaaggtcagg gctgcactgc  
61 tctcggcccc cacacggttg gttggttggc gtggtaagtg ccctgatccc tggtcctgag  
121 aactcaggct ggcacaggga ttcccagggc atctaccacc acgcagctgg agcagggctg  
181 agcccaggag catggagatg gacgccccca ggccccccag tcttgctgtc cctggagcag  
241 catcgaggcc cgggagaact gtggacaacg gaaggtcagg ccccatccat tgagttcctg  
301 gggccccact ggaggggctg ctgtggccag ggtgcacggt cacaaatgaa gacaccaagg  
361 cgcagagagg tgactcagcc tgccctcagt cacctatctg ctcttgaggg tgatccccga  
421 ctccatgagg aagcaagagg tgcggacggg cagggaggcc ggccagggcc acggtacggg  
481 ctccccagcc gagcaggtga aagccctcat ggatctgctg gctgggaagg gcagtcaagg  
541 ctccccagcc ccgcaggccc tggataggac accggatgcc ccgctggggc cctgcagcaa  
601 tgactcaagg atacagaggc accgcaaggc cctgctgagc aaggtggagg ccaccgcgg  
661 gggcgggcac ccgcccagga ccgtgcacct ggaccggctc ttcctgcctc tctcccggt  
721 gtctgtccca ccccggtct ccatcactat cggggtggcc ggcattggga agaccacct  
781 ggtgaggcac ttcgtccgcc tctgggcccc tgggcagggt ggcaaggact tctcgtggt  
841 gctgcctctg accttccggg atctcaacac ccacgagaag ctgtgtgccc accgactcat  
901 ctgctcggtc tccccgcacg tcggggagcc cagcctggcg gtggcagtcc cagccagggc  
961 cctcctgate ctggacggct tggatgagtg caggacgcct ctggacttct ccaacaccgt  
1021 ggcttcacg gacccaaaga aggagatccc ggtggaccac ctgatcacca acatcatccg  
1081 tggcaacctc tttccggaag tttccatctg gatcacctcc cgtcccagtg catctggcca  
1141 gatcccaggg ggcttgggtg accggatgac ggagatccgg ggctttaacg aggaggagat  
1201 caaggtgtgt ttggagcaga tgttccccga ggaccaggcc cttctgggct ggatgctgag  
1261 ccaagtgcag gctgacaggc ccctgtacct gatgtgcacc gtcccagcct tctgcaggct  
1321 cacgggggat gcgctaggcc acctgtggcg cagcaggacg gggccccagg atgcagagct  
1381 gtggcccccg aggacctgt gcgagctcta ctcatggtac tttaggatgg ccctcagcgg  
1441 ggaggggcag gagaagggca aggcaagccc tcgcatcgag caggtggccc atggtggccg  
1501 caagatggtg gggacattgg gccgtctggc cttccatggg ctgctcaaga agaaatacgt  
1561 gttttacgag caagacatga aggcgtttgg tgtagacctc gctctgctgc agggcgcccc  
1621 gtgcagctgc ttctgcaga gagaggagac gttggcatcg tcagtggcct actgcttcac  
1681 ccacctgtcc ctgcaggagt ttgtggcagc cgcgtattac tatggcgcat ccaggagggc  
1741 catcttcgac ctcttactg agagcggcgt atcctggccc aggctgggct tctcacgca  
1801 tttcaggagc gcagcccagc gggccatgca ggcagaggac gggaggctgg acgtgttctt  
1861 gcgcttctc tccggcctct tgtctccgag ggtcaatgcc ctctggccg gctccctgct  
1921 ggcccaaggc gagcaccagg cctaccggac ccagggtggc gagctcctgc agggctgcct  
1981 gcgccccgat gccgcagtct gtgcacgggc catcaacgtg ttgactgcc tgcattagct  
2041 gcagcacacc gagctggccc gcagcgtgga ggaggccatg gagagcgggg ccctggccag  
2101 gctgaccggt ccgcgcacc gcgctgccct agcctacctc ctgcagggtg ccgacgcctg  
2161 tgcccaggag gccaacctgt ccctgagcct cagccagggc gtccttcaga gcctgctgcc  
2221 ccagctgtct tactgccgga agctcagggt gataccaggg cagggggcag gggctgggga  
2281 aggggcagag gagagagcag aagccgtccc ctccccacca ccaagcttct ctgtcagtct  
2341 ctaggggctg ccgtaacaga ggaccatgaa cttggtggct taaaacaact aaagtgtgtt  
2401 ttctcgcagt tctggaggcc agaagtctca aatcaagggt ccaggagggc catgcgctct  
2461 ctgaaacata taggagaggt tctttccttc ctctctagct tccagtgttt gatgggaacc  
2521 cttggcttaa ggctgcgtta cttcagtctc tcccgtcgcc tggtcattct ctccctgtgt  
2581 ctgtctccac atggtgctgt cctctctttt tttttgagat ggagtccttg tctgtcgcct
```

2641 aggctggaat acagtggcgc gatctcagct cactgcaaac gctgcctcct gggttcaagc
2701 gattctcctg cctcagcctc cctagtagct gggattacag gtgcccgcc tcatgcctgg
2761 ctaatTTTTg tgTTTTtagt agagacgggg tttcaccatg ttggccaggc tgctctcaaa
2821 ctctgacct caggtgaccc gccacccca gcctcccaa ttgctgggat tacaggcctg
2881 agccactgca cctggccagt gctttcttgt cttaaaaaga cactgtcaca ctggattaca
2941 ggctcacccc acttcagcat ggccccacct taacaaagta catccacagt gacccattt
3001 ctcaataaag ccacatactt ggggcacagg gggtaggac ttcatatctt ttgtggggac
3061 acaattcaat tcataacccc ctcaaacca tccagtctga tagaagctgc acaccgctg
3121 aatgctttca gcctgtcccc tgcccgccac tctggacctt agtgagtagg gaggaagga
3181 cacaggctga gggatcatcca ggtgtccgc agaggcaggc ggtatgtggg gtggtgagga
3241 cgacagcccg tggaagatgc cgttctgcac aggaaccgca ggtctcgtgg gcaccagcc
3301 tcctgttcac tctcacggga aaggtctgag cactggggct gagcgcagat ctcagagctg
3361 cggtgatagc gctgcatggg atggagagag gcagaggccc cgggccaggg cccccacct
3421 gcccgtaggg gggtaggaca ctactgtca ctgctccct tggccaggct ggacaccaac
3481 cagttccagg acccctgat ggagctgctg ggcagcgtgc tgagtgggaa ggactgtcgc
3541 attcagaaga tcagcttggc ggagaaccag atcagtaaca aaggggccaa agctctggcc
3601 agatccctct tggtaacag aagtctgacc tctctggacc tccgcggtaa ctccattgga
3661 ccacaagggg ccaaggcgt ggcagacgct ttgaagatca accgcacct gacctccctg
3721 aggtgtgtgt cactgtctcc ctgtgttgtg accccaagag agggccaga aaacctctc
3781 ctcaggcacc acctatgaga atgggagggtg attcacaatg gcaggcatgg ggccgggcac
3841 agtggctcgc atctgtgatc ccaaagtgtg gggattacaa gtgtgagtca ccgagcccag
3901 ccagttatgt ctcttttaaa agcctgtggt tatatctata cttagctgag tgggtaccac
3961 ttttctgttc tgttttcatt tatttattta tttatttatt tatttattta tttatttatt
4021 tatttatTTT tattagggtg aaattcatgt accataaaat tgactgtttt aggcgggtcc
4081 cagaggctga tgctgtaat ccagcactt tgggaggcca aggcaggtgg atcacttgag
4141 gtcgggagtt cgagaccagc ctggccaaca tggtggaacc tcatatctac t

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42



GGTCAGGATAGGACTTCCCTCTAGAGGATCGGATCCCGGGCGCTATTATATAGTTCGATCGATCT
 TTCTCTATATATCTCCGCTATCTGATATACACACACATCCGCGGGATAGGATGACTGATCTA
 CCGCATCT
 CACAGACT

Nucleotide

My NCBI
[\[Sign In\]](#)
[\[Register\]](#)

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Limits Preview/Index History Clipboard Details

Display ☒ GenBank ☒ Show ☒ 5 ☒ Send to ☒

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [AK097030](#). Reports Homo sapiens cDNA...[gi:21756666]

[Links](#)

LOCUS AK097030 2712 bp mRNA linear PRI 30-JAN-2004
 DEFINITION Homo sapiens cDNA FLJ39711 fis, clone SMINT2013032.
 ACCESSION AK097030
 VERSION AK097030.1 GI:21756666
 KEYWORDS oligo capping; fis (full insert sequence).
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1
 AUTHORS Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R.,
 Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H.,
 Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
 Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y.,
 Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M.,
 Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
 Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T.,
 Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K.,
 Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H.,
 Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M.,
 Hiraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S.,
 Yosida,M., Hotuta,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A.,
 Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R.,
 Takeuchi,K., Arita,M., Imose,N., Musashino,K., Yuuki,H., Oshima,A.,
 Sasaki,N., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ichihara,T.,
 Shiohata,N., Sano,S., Moriya,S., Momiyama,H., Satoh,N., Takami,S.,
 Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H.,
 Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T.,
 Sugiyama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,K.,
 Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M.,
 Tashiro,H., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y.,
 Ozaki,K., Hirao,M., Ohmori,Y., Kawabata,A., Hikiji,T., Kobatake,N.,
 Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Kawakami,T.,
 Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K.,
 Nakajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togashi,T.,
 Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J.,
 Satoh,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K.,
 Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R.,
 Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.

TITLE Complete sequencing and characterization of 21,243 full-length
 human cDNAs

JOURNAL Nat. Genet. 36 (1), 40-45 (2004)
 PUBMED [14702039](#)
 REFERENCE 2

AUTHORS Tashiro,H., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S.,
Fukuzumi,Y., Fujimori,Y., Komiyama,M., Sugiyama,T., Irie,R.,
Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 2712)

AUTHORS Isogai,T. and Yamamoto,J.

TITLE Direct Submission

JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.

FEATURES Location/Qualifiers

source 1..2712
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SMINT2013032"
/tissue_type="small intestine"
/clone_lib="SMINT2"
/note="cloning vector: pME18SFL3"

ORIGIN

```

1 tttctacttt cagtttcgtg cagagcgcgagg agcgcctgagg gaggctgcac
61 tatggaaaca acctgtcaat ccagctcaag gcacacatag cccagacacc catgagaccc
121 tctccgtggg gacctagag caccatcat gaacgaggag accaaggctg gctcctcatg
181 gaccccggtg gcctccagct cggcaacaag aacctgtgga gctgtctgtg gaggctgctc
241 accaaagacc cagaatggct gaacgccaag atgaagttct tctccccaac caccgacctg
301 gattccagga acgagacctt ggacctgaa cagagagtca tctgcaact caacaagctg
361 catgtccagg gtccggacac ctggcagctt ttcattcatt gtgtgtgcat gcagctggag
421 gtgcctctgg acctggaggt gctgctgctg agtacttttg gctatgatga tgggttcacc
481 agccagctgg gagctgaggg gaaaagccaa cctgaatctc agctccacca tggcctgaag
541 cgccacatc agagctgtgg gtcctcacc cgccggaagc agtgcaagaa gcagcagcta
601 gagttggcca agaagtacct gcagctcctg cggacctctg cccagcagcg ctacaggagc
661 caaatccctg ggtcagggca gcccacgcc ttccaccagg tctatgtccc tccaatcctg
721 cgccgggcca cagcatcctt agacactctg gagggggcca ttatggggga cgtcaagggtg
781 gaagatggtg ctgacgtgag catctcggac ctcttcaaca ccagggttaa caaggccccg
841 agggtgaccg tgcttttggg gaaggctggc atgggcaaga ccacgctggc ccaccggctc
901 tgccagaagt gggcagaggg ccactctgaac tgtttccagg ccctgttctt ttttgaattc
961 cgccagctca acttgatcac gaggttctct acaccgtccg agctcctttt tgatctgtac
1021 ctgagccctg aatcggacca cgacactgtc ttccagtacc tggagaagaa cgctgaccaa
1081 gtctgtctga tctttgatgg gctagatgag gccctccagc ctatgggtcc tgatggccca
1141 ggcccagtc taccctttt ctcccatctc tgcaatggga cctcctgcc tggctgccgg
1201 gtgatggcta cctcccgtcc agggaagctg cctgcctgcc tgctgcaga ggcagccatg
1261 gtccacatgt tgggctttga tgggccacgg gtggaagaat atgtgaatca cttcttcagc
1321 gccagccat cgcgggaggg ggccctgggt gagttacaga caaatggacg tctccgaagc
1381 ctgtgtgcgg tgccgcact gtgccaagtc gcctgtctct gctccacca tctgttctc
1441 gaccagccc caggccagtc tgtggccctc ctgccaaca tgactcagct ctatatgcag
1501 atgggtgctc ccctcagccc cctggggcac ttgccacact cgtccctact ggacctgggg

```

1561 gaggtggccc tgaggggacct ggagacaggg aaggttatct tctatgcaaa agatattgct
1621 ccacccttga tagcttttgg ggccactcac agcctgctga ctctctctg cgtctgcaca
1681 ggccctgggc accagcagac aggcctatgct ttcacccacc tcagcctgca ggagtttctt
1741 gctgccctgc acctgatggc cagccccaag gtgaacaaag acacacttac ccagtatgtt
1801 accctccatt cccgctgggt acagcggacc aaagctagac tgggcctctc agaccacctc
1861 cccaccttcc tggcgggacct ggcatcctgc acctgccgcc ccttccttag ccacctggcg
1921 cagggcaatg aggactgtgt ggggtgccaag caggctgctg tagtgcagggt gttgaagaag
1981 ttggccaccc gcaagctcac agggccaaag gttgtagagc tgtgtcactg tgtggatgag
2041 acacaggagc ctgagctggc cagtctcacc gcacaaagcc tcccctatca actgcccttc
2101 cacaatttcc cactgacctg caccgacctg gccacctga ccaacatcct agagcacagg
2161 gaggcccca tccacctgga ttttgatggc tgtcccttg agccccactg ccctgaggct
2221 ctggtaggct gtgggcagat agagaatctc agctttaaga gcaggaagtg tggggatgcc
2281 tttgcagaag cctctccag gagcttgccg acaatgggga ggctgcagat gctggggtta
2341 gcaggaagta aaatcactgc ccgaggcatc agccacctgg tgaaagcttt gcctctctgt
2401 ccacagctga aagaagtcag ttttcgggac aaccagctca gtgaccagggt ggtgctgaac
2461 attgtggagg ttctccctca cctaccacgg ctccggaagc ttgacctgag cagcaacaca
2521 gacctctacc aaaaaaaaaa aaaaaaaaaa aaaaaaaatt ggtcagggtat agtggcatgc
2581 atctgtggtc ccaggattaa gggaggctga ggtgggagga tcacttgagc cggggagggtc
2641 agggttgcag tgagctgaga ttgcctcatt gcattccagc ctgggtgaca gagagaccct
2701 gtctcaaaaa ac

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42



CGCTCAGGATATGACTTCCTCCCTAGACGATCGGATCCCGGACCTATTATATAGTCGATCGATCT
TTCTCTATATCTTCCGCTATATGGGATATATACACACACATCCGGGATAGGCATGACTGATCTA
CCCACT
CAGAGACT

Nucleotide

My NCBI

[\[Sign In\]](#)

[\[Register\]](#)

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Limits

Preview/Index

History

Clipboard

Details

Display ☒ Show ☒ Send to ☒

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [AY051112](#). Reports Homo sapiens cryo...[gi:17027229]

[Links](#)

LOCUS AY051112S1 1146 bp DNA linear PRI 21-NOV-2001

DEFINITION Homo sapiens cryopyrin (CIAS1) gene, exon 1.

ACCESSION AY051112

VERSION AY051112.1 GI:17027229

KEYWORDS .

SEGMENT 1 of 8

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 1146)

AUTHORS Hoffman,H.M., Mueller,J.L., Broide,D.H., Wanderer,A.A. and Kolodner,R.D.

TITLE Mutation of a new gene encoding a putative pyrin-like protein causes familial cold autoinflammatory syndrome and Muckle-Wells syndrome

JOURNAL Nat. Genet. 29 (3), 301-305 (2001)

PUBMED [11687797](#)

REFERENCE 2 (bases 1 to 1146)

AUTHORS Hoffman,H.M., Mueller,J.L. and Kolodner,R.D.

TITLE Direct Submission

JOURNAL Submitted (15-AUG-2001) Medicine, UCSD, 9500 Gilman Drive, La Jolla, CA 92093-0635, USA

FEATURES

source Location/Qualifiers

1..1146

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="1"

/map="1q44"

gene order(<1..1146,AY051113.1:1..473,AY051114.1:1..1958,AY056059.1:1..385,AY051115.1:1..325,AY056060.1:1..411,AY051116.1:1..1305,AY051117.1:1..>480)

/gene="CIAS1"

/note="mutations can cause familial cold autoinflammatory syndrome and Muckle Wells syndrome"

mRNA join(<1..1029,AY051113.1:170..289,AY051114.1:95..1847,AY056059.1:107..277,AY051115.1:85..255,AY056060.1:92..262,AY051116.1:238..408,AY051116.1:917..1087,AY051117.1:68..>480)

/gene="CIAS1"

/product="cryopyrin"

/note="alternatively spliced; corresponds to mRNA deposited in GenBank Accession Number AF410477"

mRNA join(<1..1029,AY051113.1:170..289,AY051114.1:95..1847,
AY051115.1:85..255,AY051116.1:238..408,
AY051116.1:917..1087,AY051117.1:68..>480)
/gene="CIAS1"
/product="cryopyrin"
/note="alternatively spliced; corresponds to mRNA
deposited in GenBank Accession Number AF427617"

exon <1..1029
/gene="CIAS1"
/number=1

5'UTR <1..752
/gene="CIAS1"

CDS join(753..1029,AY051113.1:170..289,AY051114.1:95..1847,
AY056059.1:107..277,AY051115.1:85..255,AY056060.1:92..262,
AY051116.1:238..408,AY051116.1:917..1087,
AY051117.1:68..167)
/gene="CIAS1"
/note="alternatively spliced; corresponds to mRNA
deposited in GenBank Accession Number AF410477"
/codon_start=1
/product="cryopyrin"
/protein_id="AAL12497.1"
/db_xref="GI:17027237"
/translation="MASTRCKLARYLEDLEDVDLKKFKMHLEDYPPQKGCIPPLRGQT
EKADHVDLATLMIDFNGEKAWAMAVWIFAAINRRDLYEKAKRDEPKWGSNDARVSNP
TVICQEDSIEEEWMGLLEYLSRISICKMKKDYRKKYRKYVRSRQCIEDRNARLGESV
SLNKRYTRLRLIKEHRSQQEREQELLAIGKTKTCESPVSPIKMELLFDPDDEHSEPVH
TVVFQGAAGIGKTI LARKMMLDWASGTLYQDRFDYLFYIHCREVSLVTQRS LGDLIMS
CCPDNPPIHKIVRKPSRILFLMDGFDELQGA FDEHIGPLCTDWQKAERGDILLSSLI
RKKLLPEASLLITTRPVALEKLQHLLDHPRHVEILGFSEAKRKEYFFKYFSDEAQARA
AFSLIQENEVLFTMCFIPLVCWIVCTGLKQQMESGKSLAQTSKTTTAVYVFFLSSLLQ
PRGGSQEHGLCAHLWGLCSLAADGIWNQKILFEESDLRNHGLQKADVSAFLRMNLFQK
EVDCEKFYSFIHMTFQEFFAAMYLLLEEEKEGRTNVP GSRLKLP SRDVTVLL ENYGKF
EKGYLIFVVRFLFGLVNQERTSYLEKKLSCKISQQIRLELLKWIEVKAKAKKLQIQPS
QLELFYCLYEMQEEDFVQRAMDYFPKIEINLSTRMDH MVSSFCIENCHRVESLSL GFL
HNMPKEEEEEKEGRHLD MVQCVLPSSSHAACSHGLVNSHLTSSFCRGLFSVLSTSQS
LTELDLSDNSLGD PGM RVLCETLQHGPCNIRRLWLGRCLSGECCFDISLVLSSNQKL
VELDLSDNALGDFGIRLLCVGLKHL LCNLKKLWLVSCCLTSACCDLASVLTSHSLT
RLYVGENALGDSGVAILCEKAKNPQC NLQKLGLVNSGLTSVCCSALSSVLSTNQNLTH
LYLRGNTLGDKGIKLLCEGLLHPDCKLQVLELDN CNLTSHCCWDLSTLLTSSQSLRKL
SLGNNDLGD LGVM MFCEVLKQQSCLLQNLGLSEMYFNYETKSALET LQEEKPELTVVF
EPSW"

CDS join(753..1029,AY051113.1:170..289,AY051114.1:95..1847,
AY051115.1:85..255,AY051116.1:238..408,
AY051116.1:917..1087,AY051117.1:68..167)
/gene="CIAS1"
/note="alternatively spliced; corresponds to mRNA
deposited in GenBank Accession Number AF427617"
/codon_start=1
/product="cryopyrin"
/protein_id="AAL12498.1"
/db_xref="GI:17027238"
/translation="MASTRCKLARYLEDLEDVDLKKFKMHLEDYPPQKGCIPPLRGQT
EKADHVDLATLMIDFNGEKAWAMAVWIFAAINRRDLYEKAKRDEPKWGSNDARVSNP
TVICQEDSIEEEWMGLLEYLSRISICKMKKDYRKKYRKYVRSRQCIEDRNARLGESV
SLNKRYTRLRLIKEHRSQQEREQELLAIGKTKTCESPVSPIKMELLFDPDDEHSEPVH
TVVFQGAAGIGKTI LARKMMLDWASGTLYQDRFDYLFYIHCREVSLVTQRS LGDLIMS
CCPDNPPIHKIVRKPSRILFLMDGFDELQGA FDEHIGPLCTDWQKAERGDILLSSLI
RKKLLPEASLLITTRPVALEKLQHLLDHPRHVEILGFSEAKRKEYFFKYFSDEAQARA
AFSLIQENEVLFTMCFIPLVCWIVCTGLKQQMESGKSLAQTSKTTTAVYVFFLSSLLQ

PRGGSQEHGLCAHLWGLCSLAADGIWNQKILFEESDLRNHGLQKADVSAFLRMNLFQK
EVDCEKFYSFIHMTFQEFFAAMYLLLEEKEGRTNVPGRSLKLP SRDVTVLLENYGKF
EKGYLIFVVRFLFGLVNQERTSYLEKKLSCKISQQIRLELLKWIEVKAKAKKLQIQPS
QLELFYCLYEMQEEDFVQRAMDYFPKIEINLSTRMDHVMVSSFCIENCHRVESLSLGFL
HNMPKEEEEEKEGRHLD MVQC VLPSSSHAACSHGLGRCGLSHECCFDISLVLSSNQK
LVELDLSDNALGDFGIRLLCVGLKHLLCNLKKLWLVNSGLTSVCCSALSSVLSTNQNL
THLYLRGNTLGDKGIKLLCEGLLHPDCKLQVLELDNCNLTS HCCWDLSTLLTSSQSLR
KLSLGNNDLGD LGVMMFCEVLKQQSCLLQNLGLSEMYFNYETKSALETLQEEKPELTV
VFEPSW"

ORIGIN

```
1 gtagatgagg aaactgaagt tgaggaatag tgaagagttt gtccaatgtc atagccccgt
61 aatcaacggg acaaaaattht tcttgctgat gggatcaagat ggcacgtgta agtgggtggt
121 caccgtaaac tgtaatacaa tcctgtttat ggatttggtt gcatatthtt cccccatag
181 ggaaaccttt tttccatggc tcaggacaca ctctggatc gagccaacag gagaactttc
241 tggtaagcat ttggctaact tttttttttt tgagatggag tcttgctgtg tcgcctaggg
301 tggagtgcag tggcgtgatc ttggctcact gcagcctcca cctcccgggt tcaatcaatt
361 ctctacctc aacttcctga gtagctggga ttacaggcgc ccgccaccac acccggtcca
421 tttttgtact tttagtagag acacagthtt gccatgttgg ccaggctggt cttgaattcc
481 tcagctcagg tgatatgcct gccttggcct ctcaaagtgc tgggattaca ggcgtgagcc
541 actgtgcccg gccttggcta actthttcaa attaaagatt ttgactgtt acagtcattgt
601 gacatthttt tctthtctgt ttggtgagtt ttgataattt atatctctca aagtggagac
661 tttaaaaaag actcatctgt gtgccgtgtt cactgcctgg tatcttagtg tggaccgaag
721 cctaaggacc ctgaaaacag ctgcagatga agatggcaag caccgctgc aagctggcca
781 ggtacctgga ggacctggag gatgtggact tgaagaaatt taagatgcac ttagaggact
841 atctcccca gaagggtgc atccccctcc cgaggggtca gacagagaag gcagaccatg
901 tggatctagc cacgctaatt atcgacttca atggggagga gaaggcgtgg gccatggccg
961 tgtggatctt cgctgcgatc aacaggagag acctttatga gaaagcaaaa agagatgagc
1021 cgaagtgggg tgagtgggaag gaagacttht aaaaaaatt gtggccaagt gcacatagtg
1081 tacaatthtt catctthtata tatatatata tatatthtt tttttgagca cggagtgtgt
1141 cttggt
```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42

Links

deposited in GenBank Accession Number AF410477"

mRNA join(AY051112.1:<1..1029,170..289,AY051114.1:95..1847,
AY051115.1:85..255,AY051116.1:238..408,
AY051116.1:917..1087,AY051117.1:68..>480)
/gene="CIAS1"
/product="cryopyrin"
/note="alternatively spliced; corresponds to mRNA
deposited in GenBank Accession Number AF427617"

CDS join(AY051112.1:753..1029,170..289,AY051114.1:95..1847,
AY056059.1:107..277,AY051115.1:85..255,AY056060.1:92..262,
AY051116.1:238..408,AY051116.1:917..1087,
AY051117.1:68..167)
/gene="CIAS1"
/note="alternatively spliced; corresponds to mRNA
deposited in GenBank Accession Number AF410477"
/codon_start=1
/product="cryopyrin"
/protein_id="AAL12497.1"
/db_xref="GI:17027237"
/translation="MASTRCKLARYLEDLEDVDLKKFKMHLEDYPPQKGCIPLPRGQT
EKADHVDLATLMIDFNGEKAWAMAVWIFAAINRRDLYEKAKRDEPKWGSNDARVSNP
TVICQEDSIEEEWMGLLEYLSRISICKMKKDYRKRYKYVRSRFQCIEDRNARLGESV
SLNKRYTRLRLIKEHRSQQEREQELLAIGKTKTCESPVSPIKMELLFDPDDEHSEPVH
TVVFQGAAGIGKTI LARKMMLDWASGTLYQDRFDYLFYIHCREVSLVTQ RSLGDLIMS
CCPDNPPIHKIVRKPSRILFLMDGFDELQGA FDEHIGPLCTDWQKAERGDILLSSLI
RKLLPEASLLITTRPVALEKLQHLLDHPRHVEILGFSEAKRKEYFFKYFSDEAQARA
AFSLIQENEVLFTMCFIPLVCWIVCTGLKQQMESGKSLAQTSKTTTAVYVFFLSSLLQ
PRGGSQEHGLCAHLWGLCSLAADGIWNQKILFEESDLRNHGLQKADVSAFLRMNLFQK
EVDCEKFYSFIHMTFQEFFAAMYLLLEEKEGRTNVP GSRLKLP SRDVTV LLENYKGF
EKGYLIFVVRFLFGLVNQERTSYLEKKLSCKISQQIRLELLKWIEVKAKAKKLQIQPS
QLELFYCLYEMQEEDFVQRAMDYFPKIEINLSTRMDHMVSSFCIENCHRVESLSLGFL
HNMPKEEEEEKEGRHLD MVQCVLPSSSHAACSHGLVNSHLTSSFCRGLF SVLSTSQS
LTELDSLSDNSLGDPGMRVLCETLQHPGCNIRRLWLGR CGLSHECCFDISLVLSSNQKL
VELDLSDNALGDFGIRLLCVGLKHL LCNLKKLWLVS CCLTSACCQDLASVLSTSHSLT
RLYVGENALGDSGVAILCEKAKNPQC NLQKLGLVNSGLTSVCCSALSSVLSTNQNLTH
LYLRGNTLGDKGIKLLCEGLLHPDCKLQVLELDNCNL TSHCCWDLSTLLTSSQSLRKL
SLGNNDLGDLGVMMFCEVLKQQSCLLQNLGLSEMYFNYETKSALET LQEEKPELTVVF
EPSW"

CDS join(AY051112.1:753..1029,170..289,AY051114.1:95..1847,
AY051115.1:85..255,AY051116.1:238..408,
AY051116.1:917..1087,AY051117.1:68..167)
/gene="CIAS1"
/note="alternatively spliced; corresponds to mRNA
deposited in GenBank Accession Number AF427617"
/codon_start=1
/product="cryopyrin"
/protein_id="AAL12498.1"
/db_xref="GI:17027238"
/translation="MASTRCKLARYLEDLEDVDLKKFKMHLEDYPPQKGCIPLPRGQT
EKADHVDLATLMIDFNGEKAWAMAVWIFAAINRRDLYEKAKRDEPKWGSNDARVSNP
TVICQEDSIEEEWMGLLEYLSRISICKMKKDYRKRYKYVRSRFQCIEDRNARLGESV
SLNKRYTRLRLIKEHRSQQEREQELLAIGKTKTCESPVSPIKMELLFDPDDEHSEPVH
TVVFQGAAGIGKTI LARKMMLDWASGTLYQDRFDYLFYIHCREVSLVTQ RSLGDLIMS
CCPDNPPIHKIVRKPSRILFLMDGFDELQGA FDEHIGPLCTDWQKAERGDILLSSLI
RKLLPEASLLITTRPVALEKLQHLLDHPRHVEILGFSEAKRKEYFFKYFSDEAQARA
AFSLIQENEVLFTMCFIPLVCWIVCTGLKQQMESGKSLAQTSKTTTAVYVFFLSSLLQ
PRGGSQEHGLCAHLWGLCSLAADGIWNQKILFEESDLRNHGLQKADVSAFLRMNLFQK
EVDCEKFYSFIHMTFQEFFAAMYLLLEEKEGRTNVP GSRLKLP SRDVTV LLENYKGF
EKGYLIFVVRFLFGLVNQERTSYLEKKLSCKISQQIRLELLKWIEVKAKAKKLQIQPS
QLELFYCLYEMQEEDFVQRAMDYFPKIEINLSTRMDHMVSSFCIENCHRVESLSLGFL
HNMPKEEEEEKEGRHLD MVQCVLPSSSHAACSHGLGR CGLSHECCFDISLVLSSNQK

LVELDLSDNALGDFGIRLLCVGLKHLLCNLKKLWLVNSGLTSVCCSALSSVLSTNQNL
THLYLRGNTLGDKGIKLLCEGLLHPDCKLQVLELDNCNLTSHCCWDLSTLLTSSQSLR
KLSLGNNDLGDLGVMMFCEVLKQQSCLLQNLGLSEMYFNYETKSALETQEEKPELTV
VFEPSW"

exon

170..289

/gene="CIAS1"

/number=2

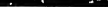


ORIGIN

```
1 gctcccaacc agacttttga ctggatacct gtcctctgca actcagagcc atgttttgat
61 ttgggggatg tttgggggtct cctctctcat gccaaatatt aggccagggt tcaattgcat
121 cctctgtgat aatagttctg ggttttgaca cttttttttt cccttttagg ttcagataat
181 gcacgtgttt cgaatcccac tgtgatatgc caggaagaca gcattgaaga ggagtggatg
241 ggtttactgg agtacctttc gagaatctct atttgtaaaa tgaagaaagg taagcgactg
301 ggggtggtgct tctagttgag ttttaagacc tgggtcagga ggctctggga agctgagcag
361 ctgggtaact tggccatact ataggttcct gctctttgga atgcaaaggc ctgtctcagg
421 aaatccattg tcagttgaag aaacaaattc atgtttgtgt ggctcttgca gtc
```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42




[\[Sign In\]](#)
[\[Register\]](#)

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Limits Preview/Index History Clipboard Details

Display **GenBank** Show **5** Send to

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

1: AY051114. Reports Homo sapiens cryo...[gi:17027231]

Links

LOCUS	AY051112S3	1958 bp	DNA	linear	PRI 21-NOV-2001
-------	------------	---------	-----	--------	-----------------

DEFINITION Homo sapiens cryopyrin (CIAS1) gene, exon 3.

ACCESSION AY051114

VERSION AY051114.1 GI:17027231

KEYWORDS

SEGMENT 3 of 8

SOURCE	Homo sapiens (human)
--------	----------------------

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 1958)

AUTHORS Hoffman, H.M., Mueller, J.L., Broide, D.H., Wanderer, A.A. and Kolodner, R.D.

TITLE Mutation of a new gene encoding a putative pyrin-like protein causes familial cold autoinflammatory syndrome and Muckle-Wells syndrome

JOURNAL Nat. Genet. 29 (3), 301-305 (2001)

PUBMED 11687797

REFERENCE 2 (bases 1 to 1958)

AUTHORS Hoffman, H.M., Mueller, J.L. and Kolodner, R.D.

TITLE Direct Submission

JOURNAL Submitted (15-AUG-2001) Medicine, UCSD, 9500 Gilman Drive, La Jolla, CA 92093-0635, USA

FEATURES	Location/Qualifiers
----------	---------------------

```
source      1..1958
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /chromosome="1"
            /map="1q44"
```

```

gene
    order (AY051112.1:<1..1146,AY051113.1:1..473,1..1958,
    AY056059.1:1..385,AY051115.1:1..325,AY056060.1:1..411,
    AY051116.1:1..1305,AY051117.1:1..>480)
    /gene="CIAS1"
    /note="mutations can cause familial cold autoinflammatory
    syndrome and Muckle Wells syndrome"

mRNA
    join (AY051112.1:<1..1029,AY051113.1:170..289,95..1847,
    AY056059.1:107..277,AY051115.1:85..255,AY056060.1:92..262,
    AY051116.1:238..408,AY051116.1:917..1087,
    AY051117.1:68..>480)
    /gene="CIAS1"
    /product="cryopyrin"
    /note="alternatively spliced; corresponds to mRNA
    deposited in GenBank Accession Number AF410477"

```

mRNA join(AY051112.1:<1..1029,AY051113.1:170..289,95..1847,
AY051115.1:85..255,AY051116.1:238..408,
AY051116.1:917..1087,AY051117.1:68..>480)
/gene="CIAS1"
/product="cryopyrin"
/note="alternatively spliced; corresponds to mRNA
deposited in GenBank Accession Number AF427617"

CDS join(AY051112.1:753..1029,AY051113.1:170..289,95..1847,
AY056059.1:107..277,AY051115.1:85..255,AY056060.1:92..262,
AY051116.1:238..408,AY051116.1:917..1087,
AY051117.1:68..167)
/gene="CIAS1"
/note="alternatively spliced; corresponds to mRNA
deposited in GenBank Accession Number AF410477"
/codon_start=1
/product="cryopyrin"
/protein_id="AAL12497.1"
/db_xref="GI:17027237"
/translation="MASTRCKLARYLEDLEDVDLKKFKMHLEDYPPQKGCIPRPGQT
EKADHVDLATLMIDFNGEKAWAMAVWIFAAINRRDLYEKAKRDEPKWGSNDARVSNP
TVICQEDSIEEEWMGLLEYLSRISICKMKKDYRKKYRKYVRSRFQCIEDRNARLGESV
SLNKRYTRLRLIKEHRSQQEREQELLAIGKTKTCESPVSPIKMELLFDPDDEHSEPVH
TVVFQGAAGIGKTI LARKMMLDWASGTLYQDRFDYLFYIHCREVSLVTQRS LGDLIMS
CCPDNPPIHKIVRKPSRILFLMDGFDELQGA FDEHIGPLCTDWQKAERGDILLSSLI
RKKLLPEASLLITTRPVALEKLQHLLDHPRHVEILGFSEAKRKEYFFKYFSDEA QARA
AFSLIQENEVLFTMCFIPLVCWIVCTGLKQQMESGKSLAQT SKTTTAVYVFFLSSLLQ
PRGGSQEHGLCAHLWGLCSLAADGIWNQKILFEESDLRNHGLQKADVSAFLRMNLFQK
EVDCEKFYSFIHMTFQEFFAAMYLLLEEKEGRTNVP GSRLKLP SRDVTVLL ENYGKF
EKGYLIFVVRFLFGLVNQERTSYLEKKLSCKISQQIRLELLK WIEVKAKAKKLQIQPS
QLELFYCLYEMQEEDFVQRAMDYFPKIEINLSTRMDH MVSSFCIENCHRVESLSLGFL
HNMPKEEEEEKEGRHLD MVQCVLPSSSHAACSHGLVNSHLTSSFCRGLFSVLSTSQS
LTELDLSDNSLGDPGM RVLCETLQHPGCNIRRLWLGR CGLSHECCFDISLVLSSNQKL
VELDLSDNALGDFGIRLLCVGLKHL LCNLKKLWLVSCCLTSACQDLASVLSTSHSLT
RLYVGENALGDSGVAILCEKAKNPQC NLQKLGLVNSGLTSVCCSALSSVLSTNQNLTH
LYLRGNTLGDKGIKLLCEGLLHPDCKLQVLELDNCNL TSHCCWDLSTLLTSSQSLRKL
SLGNNDLGDLGVMMFCEVLKQQSCLLQNLGLSEMYFNYETKSALET LQEEKPELTVVF
EPSW"

CDS join(AY051112.1:753..1029,AY051113.1:170..289,95..1847,
AY051115.1:85..255,AY051116.1:238..408,
AY051116.1:917..1087,AY051117.1:68..167)
/gene="CIAS1"
/note="alternatively spliced; corresponds to mRNA
deposited in GenBank Accession Number AF427617"
/codon_start=1
/product="cryopyrin"
/protein_id="AAL12498.1"
/db_xref="GI:17027238"
/translation="MASTRCKLARYLEDLEDVDLKKFKMHLEDYPPQKGCIPRPGQT
EKADHVDLATLMIDFNGEKAWAMAVWIFAAINRRDLYEKAKRDEPKWGSNDARVSNP
TVICQEDSIEEEWMGLLEYLSRISICKMKKDYRKKYRKYVRSRFQCIEDRNARLGESV
SLNKRYTRLRLIKEHRSQQEREQELLAIGKTKTCESPVSPIKMELLFDPDDEHSEPVH
TVVFQGAAGIGKTI LARKMMLDWASGTLYQDRFDYLFYIHCREVSLVTQRS LGDLIMS
CCPDNPPIHKIVRKPSRILFLMDGFDELQGA FDEHIGPLCTDWQKAERGDILLSSLI
RKKLLPEASLLITTRPVALEKLQHLLDHPRHVEILGFSEAKRKEYFFKYFSDEA QARA
AFSLIQENEVLFTMCFIPLVCWIVCTGLKQQMESGKSLAQT SKTTTAVYVFFLSSLLQ
PRGGSQEHGLCAHLWGLCSLAADGIWNQKILFEESDLRNHGLQKADVSAFLRMNLFQK
EVDCEKFYSFIHMTFQEFFAAMYLLLEEKEGRTNVP GSRLKLP SRDVTVLL ENYGKF
EKGYLIFVVRFLFGLVNQERTSYLEKKLSCKISQQIRLELLK WIEVKAKAKKLQIQPS
QLELFYCLYEMQEEDFVQRAMDYFPKIEINLSTRMDH MVSSFCIENCHRVESLSLGFL
HNMPKEEEEEKEGRHLD MVQCVLPSSSHAACSHGLGR CGLSHECCFDISLVLSSNQK

LVELDLSDNALGDFGIRLLCVGLKHLLCNLKKLWLVNSGLTSVCCSALSSVLSTNQNL
 THLYLRGNTLGDKGIKLLCEGLLHPDCKLQVLELDNCNLTSHCWDLSTLLTSSQSLR
 KLSLGNNDLGLGVMMFCEVLKQQSCLLQNLGLSEMYFNYETKSALETQLQEEKPELTV
 VFEPST

exon 95..1847
 /gene="CIAS1"
 /number=3

variation 289
 /gene="CIAS1"
 /note="V198M; not present in normal individuals"
 /phenotype="FCAS"
 /replace="a"

variation 752
 /gene="CIAS1"
 /note="A352V; not present in normal individuals"
 /phenotype="FCAS"
 /replace="t"

variation 1013
 /gene="CIAS1"
 /note="A439V; not present in normal individuals"
 /phenotype="FCAS"
 /replace="t"

variation 1577
 /gene="CIAS1"
 /note="E627G; not present in normal individuals"
 /phenotype="FCAS"
 /replace="g"

ORIGIN

```


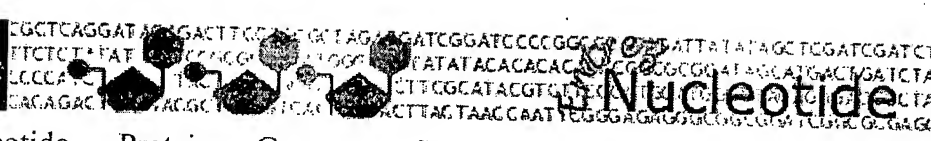
1 gttaccactc gcttccgatg acaggcccca gctgagagcg catctcaggt ggatgtgtgt
61 atactttccc cctaacttcc tgtctttgcc gtagattacc gtaagaagta cagaaagtac
121 gtgagaagca gattccagtg cattgaagac aggaatgccc gtctgggtga gagtgtgagc
181 ctcaacaaac gctacacacg actgcgtctc atcaaggagc accggagcca gcaggagagg
241 gagcaggagc ttctggccat cggcaagacc aagacgtgtg agagccccgt gagtcccatt
301 aagatggagt tgctgtttga ccccgatgat gagcattctg agcctgtgca caccgtgggtg
361 ttccaggggg cggcagggat tgggaaaaca atcctggcca ggaagatgat gttggactgg
421 gcgtcgggga cactctacca agacaggttt gactatctgt tctatatcca ctgtcgggag
481 gtgagccttg tgacacagag gagcctgggg gacctgatca tgagctgctg ccccgaccca
541 aacccaccca tccacaagat cgtgagaaaa ccctccagaa tcctcttctc catggacggc
601 ttcgatgagc tgcaaggtgc ctttgacgag cacataggac cgctctgcac tgactggcag
661 aaggccgagc ggggagacat tctcctgagc agcctcatca gaaagaagct gcttcccag
721 gcctctctgc tcatcaccac gagacctgtg gccctggaga aactgcagca cttgctggac
781 catcctcggc atgtggagat cctgggtttc tccgaggcca aaaggaaaga gtacttcttc
841 aagtacttct ctgatgaggc ccaagccagg gcagccttca gtctgattca ggagaacgag
901 gtcctcttca ccatgtgctt catccccctg gtctgctgga tcgtgtgcac tggactgaaa
961 cagcagatgg agagtggcaa gagccttgcc cagacatcca agaccaccac cgcggtgtac
1021 gtcttcttcc tttccagttt gctgcagccc cggggaggga gccaggagca cggcctctgc
1081 gcccacctct gggggctctg ctctttggct gcagatggaa tctggaacca gaaaatcctg
1141 tttgaggagt ccgacctcag gaatcatgga ctgcagaagg cggatgtgtc tgctttcctg
1201 aggatgaacc tgttccaaaa ggaagtggac tgcgagaagt tctacagctt catccacatg
1261 actttccagg agttctttgc cgccatgtac tacctgctgg aagaggaaaa ggaagggaagg
1321 acgaacgttc caggagtgct tttgaagctt cccagccgag acgtgacagt ccttctggaa
1381 aactatggca aattcgaaaa ggggtatatt atttttgttg tacgtttcct ctttggcctg
1441 gtaaacagg agaggacctc ctacttgagg aagaaattaa gttgcaagat ctctcagcaa
1501 atcaggctgg agctgctgaa atggattgaa gtgaaagcca aagctaaaaa gctgcagatc
1561 cagcccagcc agctggaatt gttctactgt ttgtacgaga tgcaggagga ggacttcgtg
1621 caaaggggcca tggactattt ccccaagatt gagatcaatc tctccaccag aatggaccac
1681 atgggtttctt ctttttgcac tgagaactgt catcgggtgg agtcaactgt cctgggggtt
1741 ctccataaca tgcccaagga ggaagaggag gaggaaaagg aaggccgaca ccttgatatg
1801 gtgcagtgtg tcctcccaag ctctctcatg gctgcctgtt ctcatgggta aggaaactcg
1861 gcttccaggt gcttctcctc gcttctctgc cagcttcttc ttggcacctg cctcctctca

```


1921 tctctttttca actatcttcc aaatactggt gccacagc
//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42

My NCBI

[PubMed](#)
[Nucleotide](#)
[Protein](#)
[Genome](#)
[Structure](#)
[PMC](#)
[Taxonomy](#)
[OMIM](#)
[Books](#)

Search for

Limits

Preview/Index

History

Clipboard

Details

Display

Range: from to
☐ Reverse complemented strand
 Features:
 ☐ SNP
 ☐ CDD
 ☒

☐ 1: [AY051115](#). Reports Homo sapiens cryo...[gi:17027233]

[Links](#)

LOCUS AY051112S5 325 bp DNA linear PRI 21-NOV-2001
DEFINITION Homo sapiens cryopyrin (CIAS1) gene, exon 5.
ACCESSION AY051115
VERSION AY051115.1 GI:17027233
KEYWORDS .
SEGMENT 5 of 8
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
REFERENCE 1 (bases 1 to 325)
AUTHORS Hoffman,H.M., Mueller,J.L., Broide,D.H., Wanderer,A.A. and
 Kolodner,R.D.
TITLE Mutation of a new gene encoding a putative pyrin-like protein
 causes familial cold autoinflammatory syndrome and Muckle-Wells
 syndrome
JOURNAL Nat. Genet. 29 (3), 301-305 (2001)
PUBMED [11687797](#)
REFERENCE 2 (bases 1 to 325)
AUTHORS Hoffman,H.M., Mueller,J.L. and Kolodner,R.D.
TITLE Direct Submission
JOURNAL Submitted (15-AUG-2001) Medicine, UCSD, 9500 Gilman Drive, La
 Jolla, CA 92093-0635, USA
FEATURES
 source Location/Qualifiers
 1..325
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="1"
 /map="1q44"
 gene order(AY051112.1:<1..1146,AY051113.1:1..473,
 AY051114.1:1..1958,AY056059.1:1..385,1..325,
 AY056060.1:1..411,AY051116.1:1..1305,
 AY051117.1:1..>480)
 /gene="CIAS1"
 /note="mutations can cause familial cold autoinflammatory
 syndrome and Muckle Wells syndrome"
 mRNA join(AY051112.1:<1..1029,AY051113.1:170..289,
 AY051114.1:95..1847,AY056059.1:107..277,85..255,
 AY056060.1:92..262,AY051116.1:238..408,
 AY051116.1:917..1087,AY051117.1:68..>480)
 /gene="CIAS1"
 /product="cryopyrin"
 /note="alternatively spliced; corresponds to mRNA"

mRNA

deposited in GenBank Accession Number AF410477"
join(AY051112.1:<1..1029,AY051113.1:170..289,
AY051114.1:95..1847,85..255,AY051116.1:238..408,
AY051116.1:917..1087,AY051117.1:68..>480)
/gene="CIAS1"
/product="cryopyrin"
/note="alternatively spliced; corresponds to mRNA

CDS

deposited in GenBank Accession Number AF427617"
join(AY051112.1:753..1029,AY051113.1:170..289,
AY051114.1:95..1847,AY056059.1:107..277,85..255,
AY056060.1:92..262,AY051116.1:238..408,
AY051116.1:917..1087,AY051117.1:68..167)
/gene="CIAS1"
/note="alternatively spliced; corresponds to mRNA
deposited in GenBank Accession Number AF410477"
/codon_start=1
/product="cryopyrin"
/protein_id="AAL12497.1"
/db_xref="GI:17027237"
/translation="MASTRCKLARYLEDLEDVDLKKFKMHLEDYPPQKGCIPPLRGQT
EKADHVDLATLMIDFNGEKAWAMAVWIFAAINRRDLYEKAKRDEPKWGSNDARVSNP
TVICQEDSIEEEWMGLLEYLSRISICKMKDYRKKYRKYVRSRQFCIEDRNARLGESV
SLNKRYTRLRLIKEHRSQQEREQELLAIGKTKTCESPVSPIKMELLFDPDDEHSEPVH
TVVFQGAAGIGKTI LARKMMLDWASGTL YQDRFDYLFYIHCREVSLVTQ RSLGDLIMS
CCPDNPPIHKIVRKPSRILFLMDGFDELQGA FDEHIGPLCTDWQKAERGDILLSSLI
RKKLLPEASLLITTRPVALEKLQHLLDHPRHVEILGFSEAKRKEYFFKYFSDEAQARA
AFSLIQENEVLFTMCFIPLVCWIVCTGLKQOMESGKSLAQTSKTTTAVYVFFLSSLLQ
PRGGSQEHGLCAHLWGLCSLAADGIWNQKILFEESDLRNHGLQKADVSAFLRMNLFQK
EVDCEKFYSFIHMTFQEFFAAMYLLLEEKEGRTNVP GSRLKLP SRDVTV LLENY GKF
EKGYLIFVVRFLFGLVNQERTSYLEKKLSCKISQQIRLELLKWIEVKAKAKKLQIQPS
QLELFYCLYEMQEEDFVQRAMDYFPKIEINLSTRMDH MVSSFCIENCHRVESLSLGFL
HNMPKEEEEEKEGRHLD MVQC VLPSSSHAACSHGLVNSHLTSSFCRGLFSVLSTSQS
LTELDLSDNSLGD PGM RVL CETLQH PGCNIRRLWLGR CGLSHECCFDISLVLSSNQKL
VELDLS DNALGDFGIRLLCVGLKHL LCNLKKLWLVSCCLTSACCDLASVLSTSHSLT
RLYVGENALGDSGVA ILC EAKNPQC NLQKLGLVNSGLTSVCCSALSSVLSTNQNLTH
LYLRGNTLGDKGIKLLCEGLLHPDCKLQVLELDN CNLTSHCCWDLSTLLTSSQSLRKL
SLGNNDLGDLGVMMFCEVLKQQSCLLQNLGLSEMYFNYETKSALET LQEEKPELT VVF
EPSW"

CDS

join(AY051112.1:753..1029,AY051113.1:170..289,
AY051114.1:95..1847,85..255,AY051116.1:238..408,
AY051116.1:917..1087,AY051117.1:68..167)
/gene="CIAS1"
/note="alternatively spliced; corresponds to mRNA
deposited in GenBank Accession Number AF427617"
/codon_start=1
/product="cryopyrin"
/protein_id="AAL12498.1"
/db_xref="GI:17027238"
/translation="MASTRCKLARYLEDLEDVDLKKFKMHLEDYPPQKGCIPPLRGQT
EKADHVDLATLMIDFNGEKAWAMAVWIFAAINRRDLYEKAKRDEPKWGSNDARVSNP
TVICQEDSIEEEWMGLLEYLSRISICKMKDYRKKYRKYVRSRQFCIEDRNARLGESV
SLNKRYTRLRLIKEHRSQQEREQELLAIGKTKTCESPVSPIKMELLFDPDDEHSEPVH
TVVFQGAAGIGKTI LARKMMLDWASGTL YQDRFDYLFYIHCREVSLVTQ RSLGDLIMS
CCPDNPPIHKIVRKPSRILFLMDGFDELQGA FDEHIGPLCTDWQKAERGDILLSSLI
RKKLLPEASLLITTRPVALEKLQHLLDHPRHVEILGFSEAKRKEYFFKYFSDEAQARA
AFSLIQENEVLFTMCFIPLVCWIVCTGLKQOMESGKSLAQTSKTTTAVYVFFLSSLLQ
PRGGSQEHGLCAHLWGLCSLAADGIWNQKILFEESDLRNHGLQKADVSAFLRMNLFQK
EVDCEKFYSFIHMTFQEFFAAMYLLLEEKEGRTNVP GSRLKLP SRDVTV LLENY GKF
EKGYLIFVVRFLFGLVNQERTSYLEKKLSCKISQQIRLELLKWIEVKAKAKKLQIQPS
QLELFYCLYEMQEEDFVQRAMDYFPKIEINLSTRMDH MVSSFCIENCHRVESLSLGFL

HNMPKEEEEEKEGRHLD MVQC VLPSSSHAACSHGLGRCGLSHECCFDISLVLSSNQK
LVELDLS DNALGDFGIRLLCVGLKHLLCNLKKLWLVNSGLTSVCCSALSSVLSTNQNL
THLYLRGNTLGDKGIKLLCEGLLHPDCKLQVLELDNCNL TSHCCWDLSTLLTSSQSLR
KLSLGNNDLGDLGVMMFCEVLKQQSCLLQNLGLSEMYFNYETKSALETLOEEKPELTV
VFEP SW"

exon

85..255

/gene="CIAS1"

/number=5


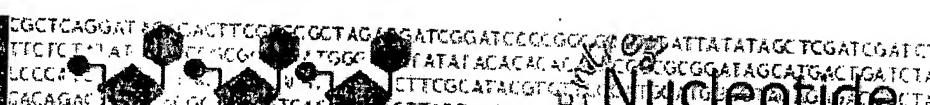
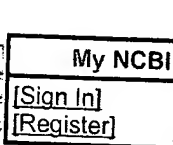
ORIGIN

1 aggtgtgtcc tgatgcttcc tctgttctgg agctctctgg tcaggtgtgt tctgatgctt
61 tctgcctctg ttcttggcat gaagggttggg gcgctgtggc ctctcgcatg agtgctgctt
121 cgacatctcc ttggtcctca gcagcaacca gaagctggtg gagctggacc tgagtgacaa
181 cgccctcggg gacttcggaa tcagacttct gtgtgtggga ctgaagcacc tgttgtgcaa
241 tctgaagaag ctctggtgag tcgagcccg tcccctaagg aagttctgcc agcgaggcgt
301 gctgcgcact ctggcttcag tgagg

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42

[PubMed](#)
[Nucleotide](#)
[Protein](#)
[Genome](#)
[Structure](#)
[PMC](#)
[Taxonomy](#)
[OMIM](#)
[Books](#)

Search for

Limits

Display

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [AY051116](#). Reports *Homo sapiens* cryo...[gi:17027235]

[Links](#)

LOCUS AY051112S7 1305 bp DNA linear PRI 21-NOV-2001
 DEFINITION *Homo sapiens* cryopyrin (CIAS1) gene, exons 7 and 8.
 ACCESSION AY051116
 VERSION AY051116.1 GI:17027235
 KEYWORDS .
 SEGMENT 7 of 8
 SOURCE *Homo sapiens* (human)
 ORGANISM *Homo sapiens*
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1305)
 AUTHORS Hoffman,H.M., Mueller,J.L., Broide,D.H., Wanderer,A.A. and
 Kolodner,R.D.
 TITLE Mutation of a new gene encoding a putative pyrin-like protein
 causes familial cold autoinflammatory syndrome and Muckle-Wells
 syndrome
 JOURNAL Nat. Genet. 29 (3), 301-305 (2001)
 PUBMED 11687797
 REFERENCE 2 (bases 1 to 1305)
 AUTHORS Hoffman,H.M., Mueller,J.L. and Kolodner,R.D.
 TITLE Direct Submission
 JOURNAL Submitted (15-AUG-2001) Medicine, UCSD, 9500 Gilman Drive, La
 Jolla, CA 92093-0635, USA
 FEATURES
 source Location/Qualifiers
 1..1305
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="1"
 /map="1q44"
 gene order(AY051112.1:<1..1146,AY051113.1:1..473,
 AY051114.1:1..1958,AY056059.1:1..385,AY051115.1:1..325,
 AY056060.1:1..411,1..1305,AY051117.1:1..>480)
 /gene="CIAS1"
 /note="mutations can cause familial cold autoinflammatory
 syndrome and Muckle Wells syndrome"
 mRNA join(AY051112.1:<1..1029,AY051113.1:170..289,
 AY051114.1:95..1847,AY056059.1:107..277,
 AY051115.1:85..255,AY056060.1:92..262,238..408,917..1087,
 AY051117.1:68..>480)
 /gene="CIAS1"
 /product="cryopyrin"
 /note="alternatively spliced; corresponds to mRNA
 deposited in GenBank Accession Number AF410477"

mRNA join(AY051112.1:<1..1029,AY051113.1:170..289,
AY051114.1:95..1847,AY051115.1:85..255,238..408,917..1087,
AY051117.1:68..>480)
/gene="CIAS1"
/product="cryopyrin"
/note="alternatively spliced; corresponds to mRNA
deposited in GenBank Accession Number AF427617"

CDS join(AY051112.1:753..1029,AY051113.1:170..289,
AY051114.1:95..1847,AY056059.1:107..277,
AY051115.1:85..255,AY056060.1:92..262,238..408,917..1087,
AY051117.1:68..167)
/gene="CIAS1"
/note="alternatively spliced; corresponds to mRNA
deposited in GenBank Accession Number AF410477"
/codon_start=1
/product="cryopyrin"
/protein_id="AAL12497.1"
/db_xref="GI:17027237"
/translation="MASTRCKLARYLEDLEDVDLKKFKMHLEDYPPQKGCIPPLRGQT
EKADHVDLATLMIDFNGEKAWAMAVWIFAAINRRDLYEKAKRDEPKWGSNDARVSNP
TVICQEDSIEEEWMGLLEYLSRISICKMKKDYRKKYRKYVRSRQCIEDRNARLGESV
SLNKRYTRLRLIKEHRSQQEREQELLAIGKTKTCESPVSPIKMELLFDPDEHSEPVH
TVVFQGAAGIGKTI LARKMMLDWASGTLYQDRFDYLFYIHCREVSLVTQ RSLGDLIMS
CCPDNPPIHKIVRKPSRILFLMDGFDELQGA FDEHIGPLCTDWQKAERGDILLSSLI
RKKLLPEASLLITTRPVALEKLQHLLDHPRHVEILGFSEAKRKEYFFKYFSDEAQARA
AFSLIQENEVLFTMCFIPLVCWIVCTGLKQQMESGKSLAQTSKTTTAVYVFFLSSLLQ
PRGGSQEHGLCAHLWGLCSLAADGIWNQKILFEESDLRNHGLQKADVSAFLRMNLFQK
EVDCEKFYSFIHMTFQEFFAAMYLLLEEKEGRTNVP GSRLKLPSRDVTVLLENYGKF
EKGYLIFVVRFLFGLVNQERTSYLEKKLSCKISQQIRLELLKWIEVKAKAKKLOIQPS
QLELFYCLYEMQEEDFVQRAMDYFPKIEINLSTRMDH MVSSFCIENCHRVESLSLGLFL
HNMPKEEEEEKEGRHLD MVQC VLPSSSHAACSHGLVNSHLTSSFCRGLFSVLSTSQS
LTELDLSDNSLGD PGM RVL CETLQHPGCNIRRLWLGR CGLSHECCFDISLVLSSNQKL
VELDLSDNALGDFGIRLLCVGLKHLLCNLKKLWL VSCCLTSACCQDLASVLSTSHSLT
RLYVGENALGDSGVA ILCEKAKNPQC NLQKLGLVNSGLTSVCCSALSSVLSTNQNLTH
LYLRGNTLGDKGIKLLCEGLLHPDCKLQVLELDNCNL TSHCCWDLSTLLTSSQSLRKL
SLGNNDLGDLGVMMFCEVLKQQSCLLQNLGLSEMYFNYETKSALETQEEKPELT VVVF
EPSW"

CDS join(AY051112.1:753..1029,AY051113.1:170..289,
AY051114.1:95..1847,AY051115.1:85..255,238..408,917..1087,
AY051117.1:68..167)
/gene="CIAS1"
/note="alternatively spliced; corresponds to mRNA
deposited in GenBank Accession Number AF427617"
/codon_start=1
/product="cryopyrin"
/protein_id="AAL12498.1"
/db_xref="GI:17027238"
/translation="MASTRCKLARYLEDLEDVDLKKFKMHLEDYPPQKGCIPPLRGQT
EKADHVDLATLMIDFNGEKAWAMAVWIFAAINRRDLYEKAKRDEPKWGSNDARVSNP
TVICQEDSIEEEWMGLLEYLSRISICKMKKDYRKKYRKYVRSRQCIEDRNARLGESV
SLNKRYTRLRLIKEHRSQQEREQELLAIGKTKTCESPVSPIKMELLFDPDEHSEPVH
TVVFQGAAGIGKTI LARKMMLDWASGTLYQDRFDYLFYIHCREVSLVTQ RSLGDLIMS
CCPDNPPIHKIVRKPSRILFLMDGFDELQGA FDEHIGPLCTDWQKAERGDILLSSLI
RKKLLPEASLLITTRPVALEKLQHLLDHPRHVEILGFSEAKRKEYFFKYFSDEAQARA
AFSLIQENEVLFTMCFIPLVCWIVCTGLKQQMESGKSLAQTSKTTTAVYVFFLSSLLQ
PRGGSQEHGLCAHLWGLCSLAADGIWNQKILFEESDLRNHGLQKADVSAFLRMNLFQK
EVDCEKFYSFIHMTFQEFFAAMYLLLEEKEGRTNVP GSRLKLPSRDVTVLLENYGKF
EKGYLIFVVRFLFGLVNQERTSYLEKKLSCKISQQIRLELLKWIEVKAKAKKLOIQPS
QLELFYCLYEMQEEDFVQRAMDYFPKIEINLSTRMDH MVSSFCIENCHRVESLSLGLFL
HNMPKEEEEEKEGRHLD MVQC VLPSSSHAACSHGLGR CGLSHECCFDISLVLSSNQK

LVELDLSDNALGDFGIRLLCVGLKHLLCNLKKLWLVNSGLTSVCCSALSSVLSTNQNL
THLYLRGNTLGDKGIKLLCEGLLHPDCKLQVLELDNCNLTSHCCWDLSTLLTSSQSLR
KLSLGNNDLGDLGVMMFCEVLKQQSCLLQNLGLSEMYFNYETKSALETQEEKPELTV
VFEPWS"

exon

238..408

/gene="CIAS1"

/number=7

exon

917..1087

/gene="CIAS1"

/number=8

ORIGIN

```
1  ttggctcttt  ctgtcggact  catacagcaa  agcatctgct  gagacatcat  ttgtgtctcc
61  tgtgacagcc  agagacagca  ggtcttgctc  tccccagatc  atatctgaga  tgctggctcc
121  tgctctctga  gctgaaggct  gcagctgctg  agagaggacg  aggcactgag  tcaaagcagc
181  tgcacaatgt  tggggaacag  ctgggtactg  aggactcttc  tcctgtcct  tctacaggtt
241  ggtgaattct  ggccttacgt  cagtctgttg  ttcagctttg  tcctcgggtac  tcagcactaa
301  tcagaatctc  acgcaccttt  acctgcgagg  caacactctc  ggagacaagg  ggatcaaact
361  actctgtgag  ggactcttgc  acccgcactg  caagcttcag  gtgttgaggt  aagtcctttg
421  gtttattaca  gcaatgagaa  cacatgggtg  ccaaggggtg  agggacgttt  aggcagagtg
481  gccacaagat  aatctgtatc  ttagaagtga  ggtgtcttct  tagtgtttgc  cttgttacag
541  gatcatggga  ctgggaggag  tccttccaga  tgatatagat  gtaggaactt  gagtccttac
601  catcacagtt  ttctgtacca  caaaaacaagg  agggcagtat  gacacttaca  ttttatggaa
661  atgtagggaa  aggcacagaa  tttggtaaat  caatgaacaa  accactgtta  ctaatttgat
721  ctgtgcaatg  cagtggattt  gaaaaagaga  gagaagaata  attaccagca  tacaaggctg
781  cttgaagcta  gttagtcttg  tgctcctgtg  cttttttttt  ttccacctga  aacaagacag
841  gctaagatgc  taaaatcttg  gggagctagg  gggatgggta  aggggacatt  ttctttaaat
901  caccoccttt  ttgcagatta  gacaactgca  acctcacgtc  aactgctgc  tgggatcttt
961  ccacacttct  gacctccagc  cagagcctgc  gaaagctgag  cctgggcaac  aatgacctgg
1021  gcgacctggg  ggtcatgatg  ttctgtgaag  tgctgaaaca  gcagagctgc  ctctgcaga
1081  acctgggggtg  agtggtgctc  gcagagatgc  ccgtggtggg  actctgagtt  ctgaggaaac
1141  gttgactggt  atcaaaatcc  aggatggctc  tcgcttcatt  tgcagccact  caagattagg
1201  ttgggcctgg  gtcagttgtg  gtggatatatt  taaaatagag  aatatggggg  taaactacac
1261  attccacttc  actgagatgg  ttagaatcac  caaggctaag  ctgga
```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42




My NCBI
[Sign In](#)
[Register](#)

[PubMed](#)
[Nucleotide](#)
[Protein](#)
[Genome](#)
[Structure](#)
[PMC](#)
[Taxonomy](#)
[OMIM](#)
[Books](#)

Search for

[Limits](#)
[Preview/Index](#)
[History](#)
[Clipboard](#)
[Details](#)

Display ☒ Show ☒ Send to ☒

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [AY051117](#). Reports Homo sapiens cryo...[gi:17027236]

[Links](#)

LOCUS AY051112S8 480 bp DNA linear PRI 21-NOV-2001
 DEFINITION Homo sapiens cryopyrin (CIAS1) gene, exon 9 and complete cds, alternatively spliced.
 ACCESSION AY051117
 VERSION AY051117.1 GI:17027236
 KEYWORDS .
 SEGMENT 8 of 8
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 480)
 AUTHORS Hoffman,H.M., Mueller,J.L., Broide,D.H., Wanderer,A.A. and Kolodner,R.D.
 TITLE Mutation of a new gene encoding a putative pyrin-like protein causes familial cold autoinflammatory syndrome and Muckle-Wells syndrome
 JOURNAL Nat. Genet. 29 (3), 301-305 (2001)
 PUBMED 11687797
 REFERENCE 2 (bases 1 to 480)
 AUTHORS Hoffman,H.M., Mueller,J.L. and Kolodner,R.D.
 TITLE Direct Submission
 JOURNAL Submitted (15-AUG-2001) Medicine, UCSD, 9500 Gilman Drive, La Jolla, CA 92093-0635, USA
 FEATURES
 source Location/Qualifiers
 1..480
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="1"
 /map="1q44"
 gene order(AY051112.1:<1..1146,AY051113.1:1..473,AY051114.1:1..1958,AY056059.1:1..385,AY051115.1:1..325,AY056060.1:1..411,AY051116.1:1..1305,1..>480)
 /gene="CIAS1"
 /note="mutations can cause familial cold autoinflammatory syndrome and Muckle Wells syndrome"
 mRNA join(AY051112.1:<1..1029,AY051113.1:170..289,AY051114.1:95..1847,AY056059.1:107..277,AY051115.1:85..255,AY056060.1:92..262,AY051116.1:238..408,AY051116.1:917..1087,68..>480)
 /gene="CIAS1"
 /product="cryopyrin"
 /note="alternatively spliced; corresponds to mRNA"

mRNA deposited in GenBank Accession Number AF410477"
join(AY051112.1:<1..1029,AY051113.1:170..289,
AY051114.1:95..1847,AY051115.1:85..255,
AY051116.1:238..408,AY051116.1:917..1087,68..>480)
/gene="CIAS1"
/product="cryopyrin"
/note="alternatively spliced; corresponds to mRNA
deposited in GenBank Accession Number AF427617"
CDS join(AY051112.1:753..1029,AY051113.1:170..289,
AY051114.1:95..1847,AY056059.1:107..277,
AY051115.1:85..255,AY056060.1:92..262,AY051116.1:238..408,
AY051116.1:917..1087,68..167)
/gene="CIAS1"
/note="alternatively spliced; corresponds to mRNA
deposited in GenBank Accession Number AF410477"
/codon_start=1
/product="cryopyrin"
/protein_id="AAL12497.1"
/db_xref="GI:17027237"
/translation="MASTRCKLARYLEDLEDVDLKKFKMHLEDYPPQKGCIPLRGQT
EKADHVDLATLMIDFNGEKAWAMAVWIFAAINRRDLYEKAKRDEPKWGS DNARVSNP
TVICQEDSIEEEWMGLLEYLSRISICKMKKDYRKKYRKYVRSRQCIEDRNARLGESV
SLNKRYTRLRLIKEHRSQQEREQELLAIGKTKTCESPVSPIKMELLFDPDDEHSEPVH
TVVFQGAAGIGKTI LARKMMLDWASGTL YQDRFDYLFYIHCREVSLVTQ RSLGDLIMS
CCPDNPPIHKIVRKPSRILFLMDGFDELQGA FDEHIGPLCTDWQKAERGDILLSSLI
RKKLLPEASLLITTRPVALEK LQHLLDHPRHVEILGFSEAKRKEYFFKYFSDEAQARA
AFSLIQENEVLFTMCFIPLVCWIVCTGLKQQMESGKSLAQTSKTTTAVYVFFLSSLLQ
PRGGSQEHGLCAHLWGLCSLAADGIWNQKILFEESDLRNHGLQKADVSAFLRMNLFQK
EVDCEKFYSFIHMTFQEFFAAMYLL EEEEEKEGRTNVP GSRLKLP SRDVTVLLENYGKF
EKGYLIFVVRFLFGLVNQERTSYLEKKLSCKISQQIRLELLKWIEVKAKAKKLQIQPS
QLELFYCLYEMQEEDFVQRAMDYFPKIEINLSTRMDH MVSSFCIENCHRVESLSLGF L
HNMPKEEEEEKEGRHLD MVQC VLPSSSHAACSHGLVNSHLTSSFCRGLFSVLSTSQS
LTELDLSDNSLGD PGM RVL CETLQHPGCNIRRLWLGR CGLSHECCFDISLVLSSNQKL
VELDLS DNALGDFGIRLLCVGLKHL LCNLKKLWL VSCCLTSACQDLASVLSTSHSLT
RLYVGENALGDSGVAILCEKAKNPQCNLQKLGLVNSGLTSVCCSALSSVLSTNQNLTH
LYLRGNTLGDKGIKLLCEGLLHPDCKLQVLELDN CNLTSHCCWDLSTLLTSSQSLRKL
SLGNNDLGDLGVMMFCEVLKQQSCLLQNLGLSEMYFNYETKSALET LQEEKPELT VVF
EPSW"
CDS join(AY051112.1:753..1029,AY051113.1:170..289,
AY051114.1:95..1847,AY051115.1:85..255,
AY051116.1:238..408,AY051116.1:917..1087,68..167)
/gene="CIAS1"
/note="alternatively spliced; corresponds to mRNA
deposited in GenBank Accession Number AF427617"
/codon_start=1
/product="cryopyrin"
/protein_id="AAL12498.1"
/db_xref="GI:17027238"
/translation="MASTRCKLARYLEDLEDVDLKKFKMHLEDYPPQKGCIPLRGQT
EKADHVDLATLMIDFNGEKAWAMAVWIFAAINRRDLYEKAKRDEPKWGS DNARVSNP
TVICQEDSIEEEWMGLLEYLSRISICKMKKDYRKKYRKYVRSRQCIEDRNARLGESV
SLNKRYTRLRLIKEHRSQQEREQELLAIGKTKTCESPVSPIKMELLFDPDDEHSEPVH
TVVFQGAAGIGKTI LARKMMLDWASGTL YQDRFDYLFYIHCREVSLVTQ RSLGDLIMS
CCPDNPPIHKIVRKPSRILFLMDGFDELQGA FDEHIGPLCTDWQKAERGDILLSSLI
RKKLLPEASLLITTRPVALEK LQHLLDHPRHVEILGFSEAKRKEYFFKYFSDEAQARA
AFSLIQENEVLFTMCFIPLVCWIVCTGLKQQMESGKSLAQTSKTTTAVYVFFLSSLLQ
PRGGSQEHGLCAHLWGLCSLAADGIWNQKILFEESDLRNHGLQKADVSAFLRMNLFQK
EVDCEKFYSFIHMTFQEFFAAMYLL EEEEEKEGRTNVP GSRLKLP SRDVTVLLENYGKF
EKGYLIFVVRFLFGLVNQERTSYLEKKLSCKISQQIRLELLKWIEVKAKAKKLQIQPS
QLELFYCLYEMQEEDFVQRAMDYFPKIEINLSTRMDH MVSSFCIENCHRVESLSLGF L

HNMPKEEEEEKEGRHLDMVQCVPSSSHAACSHGLGRCGLSHECCFDISLVLSSNQK
LVELDLSDNALGDFGIRLLCVGLKHLLCNLKKLWLVNSGLTSVCCSALSSVLSTNQNL
THLYLRGNTLGDKGIKLLCEGLLHPDCKLQVLELDNCNLTSHCCWDLSTLLTSSQSLR
KLSLGNNDLGDLGVMMFCEVLKQQSCLLQNLGLSEMYFNYETKSALETQLQEEKPELTV
VFPSW"

exon 68..>480
/gene="CIAS1"
/number=9
3'UTR 168..>480
/gene="CIAS1"
polyA signal 459..464
/gene="CIAS1"

ORIGIN

```
1 gatccctca cgactctgac agagttatct gaagagtga acccaggctt tctatttgct
61 ttacagggtt gtctgaaatg tatttcaatt atgagacaaa aagtgcgtta gaaacacttc
121 aagaagaaaa gcctgagctg accgtcgtct ttgagccttc ttggtaggag tggaaacggg
181 gctgccagac gccagtgttc tccggtccct ccagctgggg gccctcaggt ggagagagct
241 gcgatccatc caggccaaga ccacagctct gtgacccctc cggaggagtg tcggagaaga
301 gagcttgccg acgatgcctt cctgtgcaga gcttgggcat ctcttttacg ccagggtgag
361 gaagacacca ggacaatgac agcatcgggt gttgttgtca tcacagcgcc tcagttagag
421 gatgttcctc ttggtgacct catgtaatta gtcattcaa taaagcactt tctttatatt
```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42




[\[Sign In\]](#)
[\[Register\]](#)

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Limits Preview/Index History Clipboard Details

Display **GenBank** Show **5** Send to

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

□ 1: [AY056059](#). Reports *Homo sapiens* cryo...[gi:17027232]

Links

LOCUS	AY051112S4	385 bp	DNA	linear	PRI 21-NOV-2001
-------	------------	--------	-----	--------	-----------------

DEFINITION Homo sapiens cryopyrin (CIAS1) gene, exon 4.

ACCESSION AY056059

VERSION AY056059.1 GI:17027232

KEYWORDS

SEGMENT 4 of 8

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 385)

AUTHORS Hoffman, H.M., Mueller, J.L., Broide, D.H., Wanderer, A.A. and Kolodner, R.D.

TITLE Mutation of a new gene encoding a putative pyrin-like protein causes familial cold autoinflammatory syndrome and Muckle-Wells syndrome

JOURNAL Nat. Genet. 29 (3), 301-305 (2001)

PUBMED 11687797

REFERENCE 2 (bases 1 to 385)

AUTHORS Hoffman, H.M., Mueller, J.L. and Kolodner, R.D.

TITLE Direct Submission

JOURNAL Submitted (15-AUG-2001) Medicine, UCSD, 9500 Gilman Drive, La Jolla, CA 92093-0635, USA

FEATURES	Location/Qualifiers
----------	---------------------

```
source      1..385
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /chromosome="1"
            /map="1q44"
```

```
gene      order(AY051112.1:<1..1146,AY051113.1:1..473,
            AY051114.1:1..1958,1..385,AY051115.1:1..325,
            AY056060.1:1..411,AY051116.1:1..1305,
            AY051117.1:1..>480)
/gene="CIAS1"
/note="mutations can cause familial cold autoinflammatory
syndrome and Muckle Wells syndrome"
```

```
mRNA      join(AY051112.1:<1..1029,AY051113.1:170..289,  
            AY051114.1:95..1847,107..277,AY051115.1:85..255,  
            AY056060.1:92..262,AY051116.1:238..408,  
            AY051116.1:917..1087,AY051117.1:68..>480)  
/gene="CIAS1"  
/product="cryopyrin"  
/note="alternatively spliced; corresponds to mRNA"
```

mRNA
deposited in GenBank Accession Number AF410477"
join(AY051112.1:<1..1029,AY051113.1:170..289,
AY051114.1:95..1847,AY051115.1:85..255,
AY051116.1:238..408,AY051116.1:917..1087,
AY051117.1:68..>480)
/gene="CIAS1"
/product="cryopyrin"
/note="alternatively spliced; corresponds to mRNA
deposited in GenBank Accession Number AF427617"
CDS
join(AY051112.1:753..1029,AY051113.1:170..289,
AY051114.1:95..1847,107..277,AY051115.1:85..255,
AY056060.1:92..262,AY051116.1:238..408,
AY051116.1:917..1087,AY051117.1:68..167)
/gene="CIAS1"
/note="alternatively spliced; corresponds to mRNA
deposited in GenBank Accession Number AF410477"
/codon_start=1
/product="cryopyrin"
/protein_id="AAL12497.1"
/db_xref="GI:17027237"
/translation="MASTRCKLARYLEDLEDVDLKKFKMHLEDYPPQKGCIPPLPRGQT
EKADHVDLATLMIDFNGEKAWAMAVWIFAAINRRDLYEKAKRDEPKWGS DNARVSNP
TVICQEDSIEEEWMGLLEYLSRISICKMKKDYRK KYRKYVRSRFQCIEDRNARLGESV
SLNKRYTRLRLIKEHRSQQEREQELLAIGKTKTCESPVSP IKMELLFDPDDEHSEPVH
TVVFQGAAGIGK TILARKMMLDWASGTLYQDRFDYLFYIHCREVSLVTQ RSLGDLIMS
CCPDNPPIHKIVRKPSRILFLMDGFDELQGA FDEHIGPLCTDWQKAERGDILLSSLI
RKKLLPEASLLITTRPVALEKLQHLLDHPRHVEILGFSEAKRKEYFFKYFSDEAQARA
AFSLIQENEVLFTMCFIPLVCWIVCTGLKQOMESGKSLAQT SKTTTAVYVFFLSSLLQ
PRGGSQEHGLCAHLWGLCSLAADGIWNQKILFEESDLRNHGLQKADVSAFLRMNLFQK
EVDCEKFYSFIHMTFQEFFAAMYLLLEEKEGRTNVP GSRLKLP SRDVTVLLENYGKF
EKGYLIFVVRFLFGLVNQERTSYLEKKLSCKISQQIRLELLKWIEVKAKAKKLOIQPS
QLELFYCLYEMQEEDFVQRAMDYFPKIEINLSTRMDH MVSSF CIENCHRVESLSLGLF
HNMPKEEEEEKEGRHLD MVQCVP LSSSHAACSHGLVNSHLTSSFCRGLFSVLSTSQS
LTELDLSDNSLGD PGMRVLCETLQHPGCNIRRLWLGR CGLSHECCFDISLVLSSNQKL
VELDLSDNALGDFGIRLLCVGLKHL LCNLKKLWLVSCCLTSACCDLASVLSTSHSLT
RLYVGENALGDSGVAILCEKAKNPQCNLQKLGLVNSGLTSVCCSALSSVLSTNQNLTH
LYLRGNTLGDKGIKLLCEGLLHPDCKLQVLELDNCNL TSHCCWDLSTLLTSSQSLRKL
SLGNNDLGDLGVMMFCEVLKQQSCLLQNLGLSEMYFNYETKSALETLQEEKPELTVVF
EPSW"
CDS
join(AY051112.1:753..1029,AY051113.1:170..289,
AY051114.1:95..1847,AY051115.1:85..255,
AY051116.1:238..408,AY051116.1:917..1087,
AY051117.1:68..167)
/gene="CIAS1"
/note="alternatively spliced; corresponds to mRNA
deposited in GenBank Accession Number AF427617"
/codon_start=1
/product="cryopyrin"
/protein_id="AAL12498.1"
/db_xref="GI:17027238"
/translation="MASTRCKLARYLEDLEDVDLKKFKMHLEDYPPQKGCIPPLPRGQT
EKADHVDLATLMIDFNGEKAWAMAVWIFAAINRRDLYEKAKRDEPKWGS DNARVSNP
TVICQEDSIEEEWMGLLEYLSRISICKMKKDYRK KYRKYVRSRFQCIEDRNARLGESV
SLNKRYTRLRLIKEHRSQQEREQELLAIGKTKTCESPVSP IKMELLFDPDDEHSEPVH
TVVFQGAAGIGK TILARKMMLDWASGTLYQDRFDYLFYIHCREVSLVTQ RSLGDLIMS
CCPDNPPIHKIVRKPSRILFLMDGFDELQGA FDEHIGPLCTDWQKAERGDILLSSLI
RKKLLPEASLLITTRPVALEKLQHLLDHPRHVEILGFSEAKRKEYFFKYFSDEAQARA
AFSLIQENEVLFTMCFIPLVCWIVCTGLKQOMESGKSLAQT SKTTTAVYVFFLSSLLQ
PRGGSQEHGLCAHLWGLCSLAADGIWNQKILFEESDLRNHGLQKADVSAFLRMNLFQK
EVDCEKFYSFIHMTFQEFFAAMYLLLEEKEGRTNVP GSRLKLP SRDVTVLLENYGKF

EKGYLIFVVRFLFGLVNQERTSYLEKKLSCKISQQIRLELLKWIEVKAKAKKLQIQPS
QLELFYCLYEMQEEDFVQRAMDYFPKIEINLSTRMDHVMVSSFSCIENCHRVESLSLGFL
HNMPKEEEEEKEGRHLDMVQCVPSSSHAACSHGLGRCGLSHECCFDISLVLSSNQK
LVELDLSDNALGDFGIRLLCVGLKHLLCNLKKLWLVNSGLTSVCCSALSSVLSTNQNL
THLYLRGNTLGDKGIKLLCEGLLHPDCKLQVLELDNCNLTSHCWDLSTLLTSSQSLR
KLSLGNNDLGDVGMMFCEVLKQQSCLLQNLGLSEMYFNYETKSALETLOBEKPELTV
VFEPSW"

exon

107..277

/gene="CIAS1"

/number=4

ORIGIN

1 cggaaggcat ttctctgaac tgggtgccagg caccgccgcc ccagctcca gttagttatt
61 attcgaggct gatttctttt ctgtctgtct tccttctaata tcctagattg gtgaacagcc
121 acctcacttc cagtttttgc cggggcctct tttcagttct gagcaccagc cagagtctaa
181 ctgaattgga cctcagtgac aattctctgg gggaccagg gatgagagtg ttgtgtgaaa
241 cgctccagca tcctggctgt aacattcgga gattgtggtg agtccccgtg catgtgatct
301 gtgtgagtg aagttcatat gagagagaga gagagaaaca gactggagaa agatcttcag
361 gaccagggtg ctggtgtggt ttctt

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42




[\[Sign In\]](#)
[\[Register\]](#)

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books
Search Nucleotide ☒ for

[Limits](#)
[Preview/Index](#)
[History](#)
[Clipboard](#)
[Details](#)

Display **GenBank** Show **5** Send to

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [AY056060](#). Reports *Homo sapiens* cryo...[gi:17027234]

Links

LOCUS	AY051112S6	411 bp	DNA	linear	PRI 21-NOV-2001
-------	------------	--------	-----	--------	-----------------

DEFINITION Homo sapiens cryopyrin (CIAS1) gene, exon 6.

ACCESSION AY056060

VERSION AY056060.1 GI:17027234

KEYWORDS

SEGMENT 6 of 8

SOURCE	Homo sapiens (human)
--------	----------------------

ORGANISM	Homo sapiens
----------	--------------

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 411)

AUTHORS Hoffman, H.M., Mueller, J.L., Broide, D.H., Wanderer, A.A. and Kolodner, R.D.

TITLE Mutation of a new gene encoding a putative pyrin-like protein causes familial cold autoinflammatory syndrome and Muckle-Wells syndrome

JOURNAL Nat. Genet. 29 (3), 301-305 (2001)

PUBMED 11687797

REFERENCE 2 (bases 1 to 411)

AUTHORS Hoffman, H.M., Mueller, J.L. and Kolodner, R.D.

TITLE Direct Submission

JOURNAL Submitted (15-AUG-2001) Medicine, UCSD, 9500 Gilman Drive, La Jolla, CA 92093-0635, USA

FEATURES Location/Qualifiers

source

1..411

```
/organism="Homo sapiens"
```

```
/mol type="genomic DNA"
```

```
/db xref="taxon:9606"
```

```
/chromosome="1"
```

```
/map="1q44"
```

gene

```
order(AY051112.1:<1..1146,AY051113.1:1..473,  
AY051114.1:1..1958,AY056059.1:1..385,AY051115.1:1..325,  
1..411,AY051116.1:1..1305,AY051117.1:1..>480)  
/gene="CIAS1"
```

/note="mutations can cause familial cold autoinflammatory syndrome and Muckle Wells syndrome"

mRNA

```
join(AY0511112.1:<1..1029,AY0511113.1:170..289,  
AY0511114.1:95..1847,AY056059.1:107..277,  
AY0511115.1:85..255,92..262,AY0511116.1:238..408,  
AY0511116.1:917..1087,AY0511117.1:68..>480)  
/gene="CIAS1"
```

```

/product="cryopyrin"
/note="alternatively spliced; corresponds to mRNA
deposited in GenBank Accession Number AF410477"

```

mRNA join(AY051112.1:<1..1029,AY051113.1:170..289,
AY051114.1:95..1847,AY051115.1:85..255,
AY051116.1:238..408,AY051116.1:917..1087,
AY051117.1:68..>480)
/gene="CIAS1"
/product="cryopyrin"
/note="alternatively spliced; corresponds to mRNA
deposited in GenBank Accession Number AF427617"

CDS join(AY051112.1:753..1029,AY051113.1:170..289,
AY051114.1:95..1847,AY056059.1:107..277,
AY051115.1:85..255,92..262,AY051116.1:238..408,
AY051116.1:917..1087,AY051117.1:68..167)
/gene="CIAS1"
/note="alternatively spliced; corresponds to mRNA
deposited in GenBank Accession Number AF410477"
/codon_start=1
/product="cryopyrin"
/protein_id="AAL12497.1"
/db_xref="GI:17027237"
/translation="MASTRCKLARYLEDLEDVDLKKFKMHLEDYPPQKGCIPPLRGQT
EKADHVDLATLMIDFNGEKAWAMAVWIFAAINRRDLYEKAKRDEPKWGSNARVSNP
TVICQEDSIEEEWMGLLEYLSRISICKMKKDYRKKYRKYVRSRQCIEDRNARLGESV
SLNKRYTRLRLIKEHRSQQEREQELLAIGKTKTCESPVSPIKMELLFDPDEHSEPVH
TVVFQGAAGIGKTI LARKMMLDWASGTLYQDRFDYLFYIHCREVSLVTQ RSLGDLIMS
CCPDPNPPPIHKIVRKPSRILFLMDGFDELQGA FDEHIGPLCTDWQKAERGDILLSSLI
RKKLLPEASLLITTRPVALEKLQHLLDHPRHVEILGFSEAKRKEYFFKYFSDEA QARA
AFSLIQENEVLFTMCFIPLVCWIVCTGLKQQMESGKSLAQTSKTTTAVYVFFLSSLLQ
PRGGSQEHGLCAHLWGLCSLAADGIWNQKILFEESDLRNHGLQKADVSAFLRMNLFQK
EVDCEKFYSFIHMTFQEFFAAMYLLLEEKEGRTNVP GSRLKLP SRDVTVLL ENYGKF
EKGYLIFVVRFLFGLVNQERTSYLEKKLSCKISQQIRLELLKWIEVKAKAKKLQIQPS
QLELFYCLYEMQEEDFVQRAMDYFPKIEINLSTRMDH MVSSFCIENCHRVESLSLGLFL
HNMPKEEEEEKEGRHLD MVQCVP LSSSHAACSHGLVNSHLTSSFCRGLFSVLSTSQS
LTELDLSDNSLGD PGM RVL CETLQH PGCNIRRLWLGRCGLSHECCFDISLV LSSNQKL
VELDLSDNALGDFGIRLLCVGLKHLLCNLKKLWLVSCCLTSACCQDLASVLSTSHSLT
RLYVGENALGDSGVAILCEKAKNPQC NLQKLGLVNSGLTSVCCSALSSVLSTNQNLTH
LYLRGNTLGDKGIKLLCEGLLHPDCKLQVLELDNCNL TSHCCWDLSTLLTSSQSLRKL
SLGNNDLGDLGVMMFCEVLKQQSCLLQNLGLSEMYFNYETKSALET LQEEKPELTVVF
EPSW"

CDS join(AY051112.1:753..1029,AY051113.1:170..289,
AY051114.1:95..1847,AY051115.1:85..255,
AY051116.1:238..408,AY051116.1:917..1087,
AY051117.1:68..167)
/gene="CIAS1"
/note="alternatively spliced; corresponds to mRNA
deposited in GenBank Accession Number AF427617"
/codon_start=1
/product="cryopyrin"
/protein_id="AAL12498.1"
/db_xref="GI:17027238"
/translation="MASTRCKLARYLEDLEDVDLKKFKMHLEDYPPQKGCIPPLRGQT
EKADHVDLATLMIDFNGEKAWAMAVWIFAAINRRDLYEKAKRDEPKWGSNARVSNP
TVICQEDSIEEEWMGLLEYLSRISICKMKKDYRKKYRKYVRSRQCIEDRNARLGESV
SLNKRYTRLRLIKEHRSQQEREQELLAIGKTKTCESPVSPIKMELLFDPDEHSEPVH
TVVFQGAAGIGKTI LARKMMLDWASGTLYQDRFDYLFYIHCREVSLVTQ RSLGDLIMS
CCPDPNPPPIHKIVRKPSRILFLMDGFDELQGA FDEHIGPLCTDWQKAERGDILLSSLI
RKKLLPEASLLITTRPVALEKLQHLLDHPRHVEILGFSEAKRKEYFFKYFSDEA QARA
AFSLIQENEVLFTMCFIPLVCWIVCTGLKQQMESGKSLAQTSKTTTAVYVFFLSSLLQ
PRGGSQEHGLCAHLWGLCSLAADGIWNQKILFEESDLRNHGLQKADVSAFLRMNLFQK
EVDCEKFYSFIHMTFQEFFAAMYLLLEEKEGRTNVP GSRLKLP SRDVTVLL ENYGKF
EKGYLIFVVRFLFGLVNQERTSYLEKKLSCKISQQIRLELLKWIEVKAKAKKLQIQPS

QLELFYCLYEMQEEDFVQRAMDYFPKIEINLSTRMDHVMSSFCIENCHRVESLSLGFL
HNMPKEEEEEKEGRHLDVQCVPSSSHACSHGLGRCGLSHECCFDISLVLSSNQK
LVELDLSDNALGDFGIRLLCVGLKHLLCNLKKLWLVNSGLTSVCCSALSSVLSTNQNL
THLYLRGNTLGDKGIKLLCEGLLHPDCKLQVLELDNCNLTSHCCWDLSTLLTSSQSLR
KLSIGNNDLGDLGVMMFCEVLKQQSCLLQNLGLSEMYFNYETKSALETLQEEKPELTV
VFEPSW"

exon

92..262

/gene="CIAS1"

/number=6

ORIGIN

```
1 gagtagaggc agtggcaggt acgggtgctt ccttgtccat ggtggagcgt gggtagagaga
61 catgactgac attctgccat ctctatggaa ggttggtcag ctgctgcctc acatcagcat
121 gttgtcagga tcttgcacga gtattgagca ccagccattc cctgaccaga ctctatgtgg
181 gggagaaatgc cttgggagac tcaggagtcg caattttatg tgaaaaagcc aagaatccac
241 agtgtaacct gcagaaactg gggtaagtct tcatgggtgt cttaccagaa aagtaacttc
301 ttttcagagg tgaattattt ggaaaatgtg gatggggggtt actttggtca ggcagagctg
361 aaggtagagt aaggaggtaa aaacatcaga aatgctttga aggactggag g
```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42

My NCBI
[Sign In]
[Register]

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Limits Preview/Index History Clipboard Details

Display ☒ Show ☒ Send to ☒Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒☐ 1: [AY092033](#). Reports Homo sapiens NALP...[gi:20268803][Links](#)

LOCUS AY092033 3237 bp mRNA linear PRI 22-APR-2002
DEFINITION Homo sapiens NALP3 intermediate isoform (NALP3) mRNA, complete cds.
ACCESSION AY092033
VERSION AY092033.1 GI:20268803
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 3237)
AUTHORS Aganna,E., Martinon,F., Hawkins,P.N., Ross,J.B., Swan,D.C.,
Booth,D.R., Lachmann,H.J., Gaudet,R., Cotter,F.E., Thome,M.,
Hitmann,G.A., Tschopp,J. and McDermott,M.F.
TITLE Mutations in the NALP3 gene are associated with autoinflammatory
disorders distinguished by recurrent fever, cold sensitivity,
sensorineural deafness and frequent AA amyloidosis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3237)
AUTHORS Martinon,F. and Tschopp,J.
TITLE Direct Submission
JOURNAL Submitted (27-MAR-2002) Biochemistry, University of Lausanne, Ch.
des Boveresses 155, Epalinges, VD 1066, Switzerland
FEATURES
Location/Qualifiers
source 1..3237
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="peripheral blood leukocytes"
gene 1..3237
/gene="NALP3"
CDS 163..2931
/gene="NALP3"
/note="member of the NALP family of inflammatory
mediators; contains PYD, NACHT and LRR domains; contains
exons 1-3, 5 and 7-9"
/codon_start=1
/product="NALP3 intermediate isoform"
/protein_id="AAM14669.1"
/db_xref="GI:20268804"
/translation="MKMASTRCKLARYLEDVLDLKKFKMHLEDYPPQKGCIPPLPRG
QTEKADHVDLATLMIDFNGEKAWAMAVWIFAAINRRDLYEKAKRDEPKWGSDNARVS
NPTVICQEDSIEEEWMGLLEYLSRISICKMKKDYRKRYKYVRSRQCIEDRNARLGE
SVSLNKLYTRLRLIKEHRSQQEREQELLAIGKTKTCESPVSPIKMELLFDPDEHSE
VHTVVFQGAAGIGKTLARKMMLDWASGTLYQDRFDYLFYIHCREVSLVTQRSLGLDI

MSCCPDPNPPPIHKIVRKPSRILFLMDGFDELQGAFFDEHIGPLCTDWHKAERGDILLSS
LIRKKLLPEASLLITTRPVALEKLQHLLDHPRHVEILGFSEAKRKEYFFKYFSDEAQA
RAAFSLIQENEVLFTMCFIPLVCWIVCTGLKQQMESGKSLAQTSTTTAVYVFFLSSL
LQPRGGSQEHGLCAHLWGLCSLAADGIWNQKILFEESDLRNHGLQKADVSAFLRMNLF
QKEVDCEKFYSFIHMTFOEFFAAMYLLLEEEKEGRTNVPGRSLKLPDRDVTVLLENYG
KFEKGYLIFVVRFLFGLVNQERTSYLEKKLSCKISQQIRLELLKWIEVKANAKKLQIQ
PSQLELFYCLYEMQEEDFVQRAMDYFPKIEINLSTRMDHVMVSSFCIENCHRVESLSLG
FLHNMPKEEEEEKEGRHLDMVQCVPSSSSHAACSHGLGRCGLSHECCFDISLVLSSN
QKLVELDLSDNALGDFGIRLLCVGLKHLNLCNLKKLWLVNSGLTSVCCSALSSVLSTNQ
NLTHLYLRGNTLGDKGILLCEGLLHPDCKLQVLELDNCLNLTSHCCWDLSTLLTSSQS
LRKLSLGNNDLGDGLGVMFCEVLKQQSCLLQNLGLSEMYFNYETKSALETLOEEKPEL
TVVFEPWSW"

ORIGIN


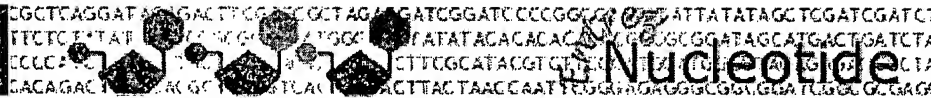
1	cttgttacag	tcatgtgaca	tttttttctt	tctgtttgct	gagtttttga	taatttatat
61	ctctcaaagt	ggagacttta	aaaagactc	atccgtgtgc	cgtgttcact	gcctggatc
121	ttagtggtga	cgaagccta	aggaccctga	aaacagctgc	agatgaagat	ggcaagcacc
181	cgctgcaagc	tggccaggta	cctggaggac	ctggaggatg	tggacttgaa	gaaatttaag
241	atgcacttag	aggactatcc	tccccagaag	ggctgcatcc	ccctcccgag	gggtcagaca
301	gagaaggcag	accatgtgga	tctagccacg	ctaagtatcg	acttcaatgg	ggaggagaag
361	gcgtgggcca	tggccgtgtg	gatcttcgct	gcatcaaca	ggagagacct	ttatgagaaa
421	gcaaaaagag	atgagccgaa	gtgggggttca	gataatgcac	gtgtttcgaa	ttccactgtg
481	atatgccagg	aagacagcat	tgaagaggag	tggatgggtt	tactggagta	cctttcgaga
541	atctctatatt	gtaaaatgaa	gaaagattac	cgtaagaagt	acagaaagta	cgtgagaagc
601	agattccagt	gcattgaaga	caggaatgcc	cgtctgggtg	agagtgtgag	cctcaacaaa
661	ctctacacac	gactgcgtct	catcaaggag	caccggagcc	agcaggagag	ggagcaggag
721	cttctggcca	tggcaagac	caagacgtgt	gagagccccg	tgagtcccat	taagatggag
781	ttgctgtttg	accccgatga	tgagcattct	gagcctgtgc	acactgtggt	gttccagggg
841	gcggcagggg	ttgggaaaac	aatcctggcc	cggaagatga	tggtggactg	ggcgtcgggg
901	acactctacc	aagacagggt	tgactatctg	ttctatatcc	actgtcggga	ggtgagcctt
961	gtgacacaga	ggagcctggg	ggacctgatc	atgagctgct	gccccgaccc	aaacccaccc
1021	atccacaaga	tctgtgagaaa	accctccaga	atcctcttcc	tcatggacgg	cttcgatgag
1081	ctgcaagggt	cctttgacga	gcacatagga	ccgctctgca	ctgactggca	taaggccgag
1141	cggggagaca	ttctcctgag	cagcctcatc	agaaagaagc	tgcttcccga	ggcctctctg
1201	ctcatcacca	cgagacctgt	ggccctggag	aaactgcagc	acttgctgga	ccatcctcgg
1261	catgtggaga	tcttggtttt	ctccgaggcc	aaaaggaaa	agtacttctt	caagtacttc
1321	tctgatgagg	cccaagccag	ggcagccttc	agtctgatcc	aggagaacga	ggtcctcttc
1381	accatgtgct	tcatccccct	ggtctgctgg	atcgtgtgca	ctggactgaa	acagcagatg
1441	gagatgggca	agagccttgc	ccagacatcc	aagaccacca	ccgcggtgta	cgtctctctc
1501	ctttccagtt	tgtgcagcc	ccggggaggg	agccaggagc	acggcctctg	cgcccacctc
1561	tgggggctct	gctctttggc	tgcagatgga	atctggaacc	agaaaatcct	gtttgaggag
1621	tccgacctca	ggaatcatgg	actgcagaag	gcggtatgtg	ctgctttcct	gaggatgaac
1681	ctgttccaaa	aggaagtgga	ctgcgagaag	ttctacagct	tcatccacat	gactttccag
1741	gagttctttg	ccgccatgta	ctacctgctg	gaagaggaaa	aggaagggaag	gacgaacgtt
1801	ccaggggagtc	gtttgaagct	ttccagccga	gacgtgacag	tccttctgga	aaactatggc
1861	aaattcgaaa	aggggtattt	gatttttgtt	gtacgtttcc	tctttggcct	ggtaaaccag
1921	gagaggacct	cctacttgga	gaagaaatta	agttgcaaga	tctctcagca	aatcaggctg
1981	gagctgctga	aatggattga	agtgaagcc	aatgctaaaa	agctgcagat	ccagcccagc
2041	cagctgggaat	tgttctactg	ttgttacgag	atgcaggagg	aggacttcgt	gcaaagggcc
2101	atggactatt	tccccaaagt	tgagatcaat	ctctccacca	gaatggacca	catggtttct
2161	tccttttgca	ttgagaactg	tcatcggtgt	gagtcactgt	ccctgggggt	tctccataac
2221	atgcccgaag	aggaagagga	ggaggaaaag	gaaggccgac	accttgatat	ggtgcagtgt
2281	gtcctcccaa	gtcctctctc	tgctgcctgt	tctcatgggt	tggggcgctg	tggcctctcg
2341	catgagtgtc	gttctgacat	ctccttggtc	ctcagcagca	accagaagct	ggtggagctg
2401	gacctgagt	acaacgcct	cggtgacttc	ggaatcagac	ttctgtgtgt	gggactgaag
2461	cacctgttgt	gcaatctgaa	gaagctctgg	ttggtgaatt	ctggccttac	gtcagtctgt
2521	tgttcagctt	tgtcctcggt	actcagcact	aatcagaatc	tcacgcacct	ttacctgcga
2581	ggcaacactc	tggagacaa	gggatcaaaa	ctactctgtg	agggactctt	gcaccccagc
2641	tgcaagcttc	aggtgttgga	attagacaac	tgcaacctca	cgtcacactg	ctgctgggat
2701	ctttccacac	ttctgacctc	cagccagagc	ctgcgaaagc	tgagcctggg	caacaatgac
2761	ctgggcgacc	tgggggtcat	gatgttctgt	gaagtgtgta	aacagcagag	ctgcctcctg

2821 cagaacctgg ggttgtctga aatgtatttc aattatgaga caaaaagtgc gttagaaaca
2881 cttcaagaag aaaagcctga gctgaccgtc gtctttgagc cttcttggtg ggagtggaaa
2941 cggggctgcc agacgccagt gttctccggt ccctccagct gggggccctc aggtggagag
3001 agctgcgatc catccaggcc aagaccacag ctctgtgatc cttccggtgg agtgtcggag
3061 aagagagctt gccgacgatg ccttcctgtg cagagcttgg gcatctcctt tacgccaggg
3121 tgaggaagac accaggacaa tgacagcatc ggggtgttgtt gtcatcacag cgcctcagtt
3181 agaggatggt cctcttggtg acctcatgta attagctcat tcaataaagc actttct

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42

My NCBI
[\[Sign In\]](#)
[\[Register\]](#)

[PubMed](#)
[Nucleotide](#)
[Protein](#)
[Genome](#)
[Structure](#)
[PMC](#)
[Taxonomy](#)
[OMIM](#)
[Books](#)

Search for

[Limits](#)
[Preview/Index](#)
[History](#)
[Clipboard](#)
[Details](#)

Display ☒ Show ☒ Send to ☒

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [AY116204](#). Reports *Homo sapiens mona...*[gi:21711820]

[Links](#)

LOCUS AY116204 3731 bp mRNA linear PRI 21-MAY-2003
 DEFINITION *Homo sapiens monarch-1 mRNA, complete cds; alternatively spliced.*
 ACCESSION AY116204
 VERSION AY116204.1 GI:21711820
 KEYWORDS .
 SOURCE *Homo sapiens* (human)
 ORGANISM *Homo sapiens*
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; *Homo*.
 REFERENCE 1 (bases 1 to 3731)
 AUTHORS Williams,K.L., Taxman,D.J., Linhoff,M.W., Reed,W. and Ting,J.P.Y.
 TITLE Monarch-1: A Pyrin/Nucleotide-Binding Domain/Leucine-Rich Repeat
 Protein That Controls Classical and Nonclassical MHC Class I Genes
 JOURNAL J. Immunol. 170 (11), 5354-5358 (2003)
 PUBMED 12759408
 REFERENCE 2 (bases 1 to 3731)
 AUTHORS Williams,K.L., Linhoff,M.W., Harton,J.A. and Ting,J.P.Y.
 TITLE Direct Submission
 JOURNAL Submitted (29-MAY-2002) Lineberger Cancer Center, UNC, Mason Farm
 Road, Chapel Hill, NC 27599, USA
 FEATURES
 Location/Qualifiers
 source 1..3731
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /chromosome="19"
 /map="19q13.4"
 /cell_line="U937"
 CDS 221..3409
 /note="alternatively spliced"
 /codon_start=1
 /product="monarch-1"
 /protein_id="AAM75142.1"
 /db_xref="GI:21711821"
 /translation="MLRTAGRDGLCRLSTYLEELEAVELKKFKLYLGTATELGEGKIP
 WGSMEKAGPLEMAQLLITHFGPEEAWRLALSTFERINRKDLWERGQREDLVRDTPPGG
 PSSLGNQSTCLLEVSLVTPRKDPQETYRDYVRRKFRLMEDRNARLGECVNLSHRYTRL
 LLVKEHSNPMQVQQQLLDTGRGHARTVGHQASPIKIETLFEPDEERPEPPRTVVMQGA
 AGIGKSMLAHKVMLDWADGKLFQGRFDYLFYINCREMNQSATECSMQDLIFSCWPEPS
 APLQELIRVPERLLFIIDGFDELKPSFHDPQGPWCWCWEEKRPTTELLNSLIRKKLLP
 ELSLITTRPTALEKLHRLLEHPRHVEILGFSEAERKEYFYKYFHNAEQAGQVFNVVR
 DNEPLFTMCFVPLVCWVVCTCLQQQLEGGGLLRQTSRTTTAVYMLYLLSLMQPKPGAP
 RLQPPPNQRGLCSLAADGLWNQKILFEEQDLRKHGLDGEDVSAFLNMNIFQKDINCER
 YYSFIHLSFQEFFAAMYIILDEGEGGAGPDQDVTRLLTEYAFSERSFLALTSRFLFGL

LNEETRSHLEKSLCWKVSPHIKMDLLQWIIQSKAQSDGSTLQQGSLEFFSCLYEIQEEE
 FIQQALSHFQVIVVSNIAASKMEHVMVSSFCLKRCRSAQVLHLYGATYSADGEDRARC
 GAHTLLVQLRPERTVLLDAYSEHLAAALCTNPNIELSLYRNALGSRGVKLLCQGLRH
 PNCKLQNLRLKRCRISSACEDLSAALIANKNLTRMDLSGNGVGFPGMMLLCEGLRHP
 QCRLQMIQLRKQLESGACQEMASVLGTNPHLVELDLTGNALEDLGLRLLCQGLRHPV
 CRLRTLWLKICRLTAAACDELASTLSVNQSLRELDLSLNLGDLGVLLLCQGLRHPTC
 KLQTLRLGICRLGSAACEGLSVVLQANHNLRDLFNDLGDWGLWLLAEGLOHPACR
 LQKLWLDSCGLTAKACENLYFTLGINQTLTDLYLTNNALGDTGVRLLCRLSHPGCKL
 RVLWLFGMDLNKMTSHRLAALRVTKPYLDIGC"

misc feature 869..892
 /note="Region: P-loop"
misc feature 2069..3406
 /note="Region: leucine rich repeat"
misc feature 221..289
 /note="Region: pyrin domain"

ORIGIN

```

1 attggtgagt ggggcagggc aggaggggaac tgaagagtga gaaagcatta tttcagcaaa
61 aggtctttcc tcccttgctc actcctccaa ccactggctc agcctctccg cccgctgcct
121 gtgaatgatg caatggaagg tgtgctgggg tcgccctgtg tcccgatcat aggagcatct
181 cagcctccag gtccctctct ttggggctta cggcaccccc atgctacgaa ccgcaggcag
241 ggacggcctc tgtcgctgt ccacctactt ggaagaactc gaggtgtgtg aactgaagaa
301 gttcaagtta tacctgggga ccgcgacaga gctgggagaa ggcaagatcc cctggggaag
361 catggagaag gccggtcccc tggaaatggc ccagctgctc atcaccactc tcggggccaga
421 ggaggcctgg aggttggtct tcagcacctt tgagcggata aacaggaagg acctgtggga
481 gagaggacag agagaggacc tggtagggga taccacacct ggtggcccggt cctcacttgg
541 gaaccagtca acatgccttc tggaaagtct tcttgtcact ccaagaaaag atccccagga
601 aacctacagg gactatgtcc gcaggaaatt ccggctcatg gaagaccgca atgcgcgcct
661 aggggaatgt gtcaacctca gccaccggta caccggctc ctgctggtga aggagcactc
721 aaaccccatg cagggtccagc agcagcttct ggacacaggg cggggacacg cgaggaccgt
781 gggacaccag gctagcccca tcaagataga gacctctttt gagccagacg aggagcgccc
841 cgagccaccg cgcaccgtgg tcatgcaagg cgcggcaggg ataggcaagt ccatgctggc
901 acacaagggt atgctggact gggcggacgg gaagctcttc caaggcagat ttgattatct
961 cttctacatc aactgcaggg agatgaacca gagtgccacg gaatgcagca tgcaagacct
1021 catcttcagc tgctggcctg agcccagcgc gcctctccag gagctcatcc gagttcccga
1081 gcgcctcctt ttcctcatcg acggcttcga tgagctcaag ccttctttcc acgatcctca
1141 gggaccctgg tgctctgtct gggaggagaa acggcccacg gagctgtctt ttaacagctt
1201 aattcggaag aagctgtctc ctgagctatc ttgtctatc accacacggc ccacggcttt
1261 ggagaaagct caccgtctgc tggagacccc caggcatgtg gagatcctgg gcttctctga
1321 ggcagaaaagg aaggaaatac tctacaagta tttccacaat gcagagcagg cgggccaagt
1381 cttcaattac gtgagggaca acgagcctct cttaccatg tgcttcgtcc ccctggtgtg
1441 ctgggtggtg tgtacctgcc tccagcagca gctggagggt ggggggctgt tgagacagac
1501 gtccaggacc accactgcag tgtacatgct ctacctgtg agtctgatgc aacccaagcc
1561 gggggccccc cgctccagc cccaccccaa ccagagaggg ttgtgctcct tggcggcaga
1621 tgggctctgg aatcagaaaa tcctatttga ggagcaggac ctccggaagc acggcctaga
1681 cggggaagac gtctctgcct tcctcaacat gaacatcttc cagaaggaca tcaactgtga
1741 gaggtactac agcttcatcc acttgagttt ccaggaattc tttgcagcta tgtactatat
1801 cctggacgag ggggagggcg gggcaggccc agaccaggac gtgaccaggc tgttgaccga
1861 gtacgcgttt tctgaaagga gcttcctggc actcaccagc cgcttctgtt ttggactcct
1921 gaacgaggag accaggagcc acctggagaa gagtctctgc tgggaaggct cgccgcacat
1981 caagatggac ctggtgcagt ggatccaaag caaagctcag agcgacggct ccaccctgca
2041 gcagggtctc ttggagttct tcagctgctt gtacgagatc caggaggagg agtttatcca
2101 gcaggccctg agccacttcc aggtgatcgt ggtcagcaac attgcctcca agatggagca
2161 catggtctcc tcgttctgtc tgaagcgctg caggagcgcc cagggtgtgc acttgatagg
2221 cgccacctac agcgcgagc ggggaagacc cgcgaggtgc tccgcaggag cgcacacgct
2281 gttggtgcag ctgagaccag agaggaccgt tctgctggac gcctacagtg aacatctggc
2341 agcggccctg tgcaccaatc caaacctgat agagctgtct ctgtaccgaa atgccctggg
2401 cagccggggg gtgaagctgc tctgtcaagg actcagacac cccaactgca aacttcagaa
2461 cctgagctgt aagaggtgct gcatctccag ctgagcctgc gaggacctct ctgcagctct
2521 catagccaat aagaatttga caaggatgga tctcagtggt aacggcggtg gattcccagg
2581 catgatgctg ctttgcgagg gcctgcggca tccccagtc aggctgcaga tgattcagtt

```

2641 gaggaagtgt cagctggagt ceggggcttg tcaggagatg gcttctgtgc tcggcaccaa
2701 cccacatctg gttgagttgg acctgacagg aaatgcactg gaggatttgg gcctgaggtt
2761 actatgccag ggactgaggc acccagtctg cagactacgg actttgtggc tgaagatctg
2821 ccgcctcact gctgctgcct gtgacgagct ggcctcaact ctgagtgtga accagagcct
2881 gagagagctg gacctgagcc tgaatgagct gggggacctc ggggtgctgc tgctgtgtga
2941 gggcctcagg catcccacgt gcaagctcca gaccctgcgg ttgggcatct gccggctggg
3001 ctctgccgcc tgtgaggggc tttctgtggg gctccaggcc aaccacaacc tccgggagct
3061 ggacttgagt ttcaacgacc tgggagactg gggcctgtgg ttgctggctg aggggctgca
3121 acatcccgcc tgcagactcc agaaactgtg gctggatagc tgtggcctca cagccaaggc
3181 ttgtgagaat ctttacttca ccctggggat caaccagacc ttgaccgacc tttacctgac
3241 caacaacgcc ctaggggaca caggtgtccg actgctttgc aagcggctga gccatcctgg
3301 ctgcaaaactc cgagtcctct gggtatttgg gatggacctg aataaaatga cccacagtag
3361 gttggcagcg cttcgagtaa caaaacctta tttggacatt ggctgctgaa tggtcctatc
3421 tgctggctct cccctgagat ctggacagag gaagatggga gggtgctcat cccccccca
3481 gcataatgat cagcctcctt cctagagaca gactcatgca gattgagatc aaaagtccct
3541 ctgcttggga tcaaattaat gtttgacaga gctggccagg cgtggtggct catgtatgta
3601 atcctagcac ttcgagaggc cgaggcaggt ggatcacgag gtcaggagtt tgagattagc
3661 ctggccaaga tgggtgaaacc ctgtctctac taaaaataaa aaaaaattag ccaggaaaaa
3721 aaaaaaaaaa a

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42



CGCTCAGGATAGAGACTTCGCTAGAGATCGGATCCCGGCGCGATTATATATATATCGATCGATC
TCTCTATATCCCGGCGCGATTATATACACACACACCGCGCGGATAGATACATGATCTA
CCGCTCAGGATAGAGACTTCGCTAGAGATCGGATCCCGGCGCGATTATATATATATCGATCGATC
CACAGACTTCGCTAGAGACTTCGCTAGAGATCGGATCCCGGCGCGATTATATATATATCGATCGATC

Nucleotide

My NCBI
[Sign In](#)
[Register](#)

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Limits Preview/Index History Clipboard Details

Display ☒ Show ☒ Send to

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [AY116205](#). Reports Homo sapiens mona...[gi:21711822]

[Links](#)

LOCUS AY116205 3563 bp mRNA linear PRI 21-MAY-2003

DEFINITION Homo sapiens monarch-1 splice form II mRNA, complete cds;
alternatively spliced.

ACCESSION AY116205

VERSION AY116205.1 GI:21711822

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 3563)

AUTHORS Williams,K.L., Taxman,D.J., Linhoff,M.W., Reed,W. and Ting,J.P.Y.

TITLE Monarch-1: A Pysin/Nucleotide-Binding Domain/Leucine-Rich Repeat
Protein That Controls Classical and Nonclassical MHC Class I Genes
J. Immunol. 170 (11), 5354-5358 (2003)

J. Immunol. 170 (11), 5354-5358 (2003)

PUBMED 12759408

REFERENCE 2 (bases 1 to 3563)

AUTHORS Williams,K.L., Linhoff,M.W. and Ting,J.P.Y.

TITLE Direct Submission

JOURNAL Submitted (29-MAY-2002) Lineberger Cancer Center, UNC, Mason Farm
Road, Chapel Hill, NC 27599, USA

FEATURES Location/Qualifiers

source 1..3563

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/chromosome="19"

/map="19q13.4"

/cell_line="U937"

CDS 221..3241

/note="contains alternatively spliced exon 9"

/codon_start=1

/product="monarch-1 splice form II"

/protein_id="AAM75143.1"

/db_xref="GI:21711823"

/translation="MLRTAGRDGLCRLSTYLEELEAVELEKFKLYLGTATELGEGKIP
WGSMEKAGPLEMAQLLITHFGPEEAWRLALSTFERINRKDLWERGQREDLVRDTPPGG
PSSLGNQSTCLLEVSLVTPRKDPQETRYDYVRRKFRMLMEDRNARLGECVNLSHRYTRL
LLVKEHSNPMQVQQQLLDTGRGHARTVGHQASPIKIETLFEPDEERPEPPRTVVMQGA
AGIGKSMLAHKVMLDWDAGKLFQGRFDYLFYINCREMNQSATECSMQDLIFSCWPEPS
APLQELIRVPERLLFIIDGFDELKPSFHDPPQGPWCLCWEKRPTELLNSLIRKKLLP
ELSLITTRPTALEKLHRLLEHPRHVEILGFSEAERKEYFYKYFHNAEQAGQVFNYVR
DNEPLFTMCFVPLVCWVVTCLQQQLEGGGLLRQTSRTTTAVYMLYLLSLMQPKPGAP
RLQPPPNQRGLCSLAADGLWNQKILFEEQDLRKHGLDGEDVSAFLNMNIFQKDINCR

YYSFIHLSFQEFFAAMYYILDEGEGGAGPDQDVTRLLTEYAFSERSFLALTSRFLFGL
LNEETRSHLEKSLCWKVSPIKMDLLQWIQSKAQSDGSTLQOQSLEFFSCLYEIQEEE
FIQQALSHFQVIVVSNIAASKMEHMOVSSFLKRCRSAQVLHLYGATYSADGEDRARC
GAHTLLVQLRPERTVLLDAYSEHLAAALCTNPNIELSLYRNALGSRGVKLLCQGLRH
PNCKLQNLRLKRCRISSACEDLSAALIANKNLTRMDLSGNGVGFPGMMLLCQGLRHP
QCRLQMIQLRKQLESGACQEMASVLGTNPHLVELDLTGNALEDLGLRLLCQGLRHPV
CRLRTLWLKICRLTAAACDELASTLSVNQSLRELDLSLNLGDLGVLLLCQGLRHPTC
KLQTLRLGICRLGSAACEGLSVVLQANHNRELDLSFNDLGDWGLWLLAEGHQHPACR
LQKLWWLFGMDLNKMTSRLAALRVTKPYLDIGC"

misc feature 869..892
/note="Region: P-loop"
misc feature 2069..3238
/note="Region: leucine rich repeat"
misc feature 221..289
/note="Region: pyrin domain"

ORIGIN

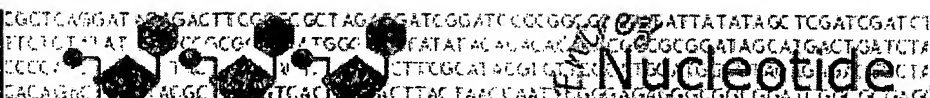

```
1 attggtgagt ggggcagggc aggagggaac tgaagagtga gaaagcatta tttcagcaaa
61 aggtctttcc tcccttgctc actcctccaa ccactggctc agcctctccg cccgctgcct
121 gtgaatgatg caatggaagg tgtgctgggg tcgccctgtg tcccgatcat aggagcatct
181 cagcctccag gtcctctcct ttggggctta cggcaccccc atgctacgaa ccgcaggcag
241 ggacggcctc tgtcgctgtt ccacctactt ggaagaactc gaggtgtgtg aactgaagaa
301 gttcaagtta tacctgggga ccgcgacaga gctgggagaa ggcaagatcc cctggggaag
361 catggagaag gccggtcccc tggaaatggc ccagctgctc atcaccactc tcgggcccaga
421 ggaggcctgg aggttggctc tcagcacctt tgagcggata aacaggaagg acctgtggga
481 gagaggacag agagaggacc tgggtaggga taccacactt ggtggcccggt cctcacttgg
541 gaaccagtca acatgccttc tggaaagtctc tcttgctact ccaagaaaag atccccagga
601 aacctacagg gactatgtcc gcaggaaatt ccggctcatg gaagaccgca atgcgcgcct
661 aggggaatgt gtcaacctca gccaccggtg caccggctc ctgctggtga aggagcactc
721 aaaccccatg cagggtccagc agcagcttct ggacacaggc cggggacacg cgaggaccgt
781 gggacaccag gctagcccca tcaagataga gaccctcttt gagccagacg aggagcgccc
841 cgagccaccg cgcaccgtgg tcatgcaagg cgcgccaggg ataggcaagt ccatgctggc
901 acacaagggt atgctggact gggcggacgg gaagctcttc caaggcagat ttgattatct
961 cttctacatc aactgcaggg agatgaacca gagtgccacg gaatgcagca tgcaagacct
1021 catcttcagc tgctggcctg agcccagcgc gcctctccag gagctcatcc gagttcccga
1081 gcgcctcctt ttcattcatc acggcttcga tgagctcaag ccttctttcc acgatcctca
1141 gggaccctgg tgctctgctt gggaggagaa acggcccacg gagctgcttc ttaacagctt
1201 aattcggaag aagctgctcc ctgagctatc tttgctcatc accacacggc ccacggcttt
1261 ggagaagaag caccgtctgc tggagacacc caggcatgtg gagatcctgg gcttctctga
1321 ggcagaaagg aaggaaatac tctacaagta tttccacaat gcagagcagg cggggcaagt
1381 cttcaattac gtgaggggaca acgacgtctc cttcaccatg tgcttcgctc ccttggtgtg
1441 ctgggtggtg tgtacctgcc tccagcagca gctggagggt ggggggctgt tgagacagac
1501 gtccaggacc accactgcag tgtacatgct ctacctgctg agtctgatgc aacccaagcc
1561 gggggccccc cgctccagc ccccacccaa ccagagaggg ttgtgctcct tggcggcaga
1621 tgggctctgg aatcagaaaa tcctatttga ggagcaggac ctccggaagc acggcctaga
1681 cggggaagac gtctctgcct tcctcaacat gaacatcttc cagaaggaca tcaactgtga
1741 gaggtactac agcttcatcc acttgagttt ccaggaattc tttgcagcta tgtactatat
1801 cctggacgag ggggagggcg gggcaggccc agaccaggac gtgaccaggc tgttgaccga
1861 gtacgcgttt tctgaaagga gcttcctggc actcaccagc cgcttctgtt ttggactcct
1921 gaacgaggag accaggagcc acctggagaa gagtctctgc tggaaaggtc cgccgcacat
1981 caagatggac ctggtgcagt ggatccaaag caaagctcag agcgacggct ccacctgca
2041 gcagggtccc ttggagttct tcagctgctt gtacgagatc caggaggagg agtttatcca
2101 gcaggccctg agccacttcc aggtgatcgt ggtcagcaac attgcctcca agatggagca
2161 catggtctcc tcgttctgtc tgaagcgctg caggagcgcc cagggtgctg acttgatagg
2221 cgccacctac agcgcgagc ggggaagacc cgcgagggtg tccgcaggag cgcacacgct
2281 gttggtgcag ctcagaccag agaggaccgt tctgctggac gcctacagtg aacatctggc
2341 agcggccctg tgcaccaatc caaacctgat agagctgtct ctgtaccgaa atgccctggg
2401 cagccggggg gtgaagctgc tctgtcaagg actcagacac cccaactgca aacttcagaa
2461 cctgaggctg aagaggtgcc gcatctccag ctcagcctgc gaggacctct ctgcagctct
2521 catagccaat aagaatttga caaggatgga tctcagtggc aacggcggtg gattcccagg
2581 catgatgctg ctttgcgagg gcctgcggca tccccagtgc aggctgcaga tgattcagtt
```


2641 gaggaagtgt cagctggagt ccggggccttgc tcaggagatg gcttctgtgc tcggcaccaa
2701 cccacatctg gttgagttgg acctgacagg aaatgcactg gaggatttgg gcctgaggtt
2761 actatgccag ggactgaggc acccagtctg cagactacgg actttgtggc tgaagatctg
2821 ccgcctcact gctgctgcct gtgacgagct ggcctcaact ctcagtgtga accagagcct
2881 gagagagctg gacctgagcc tgaatgagct gggggacctc ggggtgctgc tgctgtgtga
2941 gggcctcagg catcccacgt gcaagctcca gacctgcgg ttgggcatct gccggctggg
3001 ctctgccgcc tgtgagggtc tttctgtggg gctccaggcc aaccacaacc tccgggagct
3061 ggacttgagt ttcaacgacc tgggagactg gggcctgtgg ttgctggctg aggggctgca
3121 acatcccgcc tgcagactcc agaaactgtg gtggttattt gggatggacc tgaataaaat
3181 gacccacagt aggttggcag cgcttcgagt aacaaaacct tatttggaca ttggctgctg
3241 aatggtccta tctgctggct ctcccctgag atctggacag aggaagatgg gagggtgctc
3301 atcacccccc cagcataatg atcagcctcc ttcctagaga cagactcatg cagattgaga
3361 tcaaaagtcc ctctgcttgg gatcaaatta atgtttgaca gagctggcca ggcgtggtgg
3421 ctcatgtatg taatcctagc acttcgagag gccgaggcag gtggatcacg aggtcaggag
3481 tttgagatta gcctggccaa gatggtgaaa ccctgtctct actaaaaata aaaaaaaatt
3541 agccaggaaa aaaaaaaaaa aaa

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42



My NCBI
[\[Sign In\]](#)
[\[Register\]](#)

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books
Search for

Limits Preview/Index History Clipboard Details

Display

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [AY116206](#). Reports Homo sapiens mona...[gi:21711824]

[Links](#)

LOCUS AY116206 3395 bp mRNA linear PRI 21-MAY-2003

DEFINITION Homo sapiens monarch-1 splice form III mRNA, complete cds;
alternatively spliced.

ACCESSION AY116206

VERSION AY116206.1 GI:21711824

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM [Homo sapiens](#)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 3395)

AUTHORS Williams,K.L., Taxman,D.J., Linhoff,M.W., Reed,W. and Ting,J.P.Y.

TITLE Monarch-1: A Pyrin/Nucleotide-Binding Domain/Leucine-Rich Repeat
Protein That Controls Classical and Nonclassical MHC Class I Genes
J. Immunol. 170 (11), 5354-5358 (2003)

JOURNAL 12759408

REFERENCE 2 (bases 1 to 3395)

AUTHORS Williams,K.L., Linhoff,M.W. and Ting,J.P.Y.

TITLE Direct Submission

JOURNAL Submitted (29-MAY-2002) Lineberger Cancer Center, UNC, Mason Farm
Road, Chapel Hill, NC 27599, USA

FEATURES Location/Qualifiers

source 1..3395
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="19"
/map="19q13.4"

CDS 221..3073
/note="contains alternatively spliced exons 7 and 8"
/codon_start=1

/product="monarch-1 splice form III"
/protein_id="[AAM75144.1](#)"
/db_xref="GI:21711825"
/translation="MLRTAGRDGLCRLSTYLEELEAVELEKKFKLYLGTATELGEGKIP
WGSMEKAGPLEMAQLLITHFGPEEAWRLALSTFERINRKDLWERGQREDLVRDTPPGG
PSSLGNQSTCLLEVSLVTPRKDPQETRYDYVRRKFRMLMEDRNARLGECVNLSHRYTRL
LLVKEHSNPMQVQQQLLDTGRGHARTVGHQASPIKIETLFEPEDEERPEPPRTVVMQGA
AGIGKSMLAHKVMLDWADGKLFQGRFDYLFYINCREMNQSADECSMQDLIFSCWPEPS
APLQELIRVPERLLFIIDGFDELKPSFHDPQGPWCWCWEEKRPTTELLNSLIRKKLLP
ELSLITTRPTALEKLHRLLEHPRHVEILGFSEAERKEYFYKYFHNAEQAGQVFNVVR
DNEPLFTMCFVPLVCWVVTCLQQQLEGGGLLRQTSRTTTAVYMLYLLSLMQPKPGAP
RLQPPPNQRGLCSLAADGLWNQKILFEEQDLRKHGLDGEDVSAFLNMNIFQKDINCER
YYSFIHLSFQEFFAAMYYILDEGEGGAGPDQDVTRLLTEYAFSERSFLALTSRFLFGL

LNEETRSHLEKSLCWKVSPHIKMDLLQWIQSKAQSDGSTLQQGSLEFFSCLYEIQEEE
FIQQALSHFQVIVVSNIAASKMEHVMVSSFCLKRCRSAQVLHLYGATYSADGEDRARC
GAHTLLVQLRPERTVLLDAYSEHLAAALCTNPNIELSLYRNALGSRGVKLLCQGLRH
PNCKLQNLRLKRCRISSACEDLSAALIANKNLTRMDLSGNGVGFPGMMLLCEGLRHP
QCRLQMIQLRKQLESGACQEMASVLGTNPHLVELDLTGNALEDLGLRLLCQGLRHPV
CRLRTLWLWLDSCGLTAKACENLYFTLGINQTLTDLYLTNNALGDTGVRLLCKRLSHP
GCKLRVLWLFGMDLNKMTSRLAALRVTKPYLDIGC"

misc feature 869..892
/note="Region: P-loop"
misc feature 2069..3070
/note="Region: leucine rich repeat"
misc feature 221..289
/note="Region: pyrin domain"

ORIGIN

```
1 attggtgagt ggggcagggc aggagggaac tgaagagtga gaaagcatta tttcagcaaa
61 aggtctttcc tcccttgctc actcctccaa ccactggctc agcctctccg cccgctgcct
121 gtgaatgatg caatggaagg tgtgctgggg tcgccctgtg tcccgtgcat aggagcatct
181 cagcctccag gtcctctcct ttggggctta cggcaccccc atgctacgaa ccgcaggcag
241 ggacggcctc tgtcgctgtt ccacctactt ggaagaactc gaggtgtgtg aactgaagaa
301 gttcaagtta tacctgggga ccgcgacaga gctgggagaa ggcaagatcc cctggggaag
361 catggagaag gccggtcccc tggaaatggc ccagctgctc atcacccact tcggggccaga
421 ggaggcctgg aggttggttc tcagcacctt tgagcggata aacaggaagg acctgtggga
481 gagaggacag agagaggacc tgggtaggga taccacacct ggtggcccggt cctcacttgg
541 gaaccagtca acatgccttc tggaaagtct tcttgtcact ccaagaaaag atccccagga
601 aacctacagg gactatgtcc gcaggaaatt ccggctcatg gaagaccgca atgcgcgcct
661 aggggaatgt gtcaacctca gccaccggta caccgggctc ctgctggtga aggagcactc
721 aaaccccatg cagggtccagc agcagcttct ggacacaggc cggggacacg cgaggaccgt
781 gggacaccag gctagcccca tcaagataga gaccctcttt gagccagacg aggagcgccc
841 cgagccaccg cgcaccgtgg tcatgcaagg cgcggcaggg ataggcaagt ccatgctggc
901 acacaaggtg atgctggact gggcggacgg gaagctcttc caaggcagat ttgattatct
961 cttctacatc aactgcaggg agatgaacca gagtgccacg gaatgcagca tgcaagacct
1021 catcttcagc tgctggcctg agcccagcgc gcctctccag gagctcatcc gagttcccga
1081 gcgcctcctt ttcacatcgc acggcttcga tgagctcaag ccttctttcc acgatacctca
1141 gggaccctgg tgctctgtct gggaggagaa acggcccacg gagctgtctc ttaacagctt
1201 aattcggaag aagctgctcc ctgagctatc tttgctcatc accacacggc ccacggcttt
1261 ggagaaggtc caccgtctgc tggagacccc caggcatgtg gagatcctgg gcttctctga
1321 ggcagaaagg aaggaaatac tctacaagta tttccacaat gcagagcagg cgggccaagt
1381 cttcaattac gtgagggaca acgagcctct cttcaccatg tgcttcgtcc ccttgggtgtg
1441 ctgggtggtg tgtacctgcc tccagcagca gctggagggt ggggggctgt tgagacagac
1501 gtccaggacc accactgcag tgtacatgct ctacctgtg agtctgatgc aacccaagcc
1561 gggggccccc cgctccagc ccccacccaa ccagagaggg ttgtgtcctt tggcggcaga
1621 tgggctctgg aatcagaaaa tcctatttga ggagcaggac ctccggaagc acggcctaga
1681 cggggaagac gtctctgcct tcctcaacat gaacatcttc cagaaggaca tcaactgtga
1741 gaggtactac agcttcatcc acttgagttt ccaggaattc tttgcagcta tgtactatat
1801 cctggacgag ggggagggcg gggcaggccc agaccaggac gtgaccaggc tgttgaccga
1861 gtacgcgttt tctgaaagga gcttcctggc actcaccagc cgcttcctgt ttggactcct
1921 gaacgaggag accaggagcc acctggagaa gagtctctgc tggaaaggtct cgccgcacat
1981 caagatggac ctggttcagt ggatccaaag caaagctcag agcgacggct ccaccctgca
2041 gcagggtccc ttggagttct tcagctgctt gtacgagatc caggaggagg agtttatcca
2101 gcaggccctg agccacttcc aggtgatcgt ggtcagcaac attgcctcca agatggagca
2161 catggtctcc tcgttctgtc tgaagcgctg caggagcgcc cagggtgtgc acttgatagg
2221 cgccacctac agcgcggacg gggaagaccg cgcgaggtgc tccgcaggag cgcacacgct
2281 gttggtgcag ctcagaccag agaggaccgt tctgctggac gcctacagtg aacatctggc
2341 agcggccctg tgcaccaatc caaacctgat agagctgtct ctgtaccgaa atgccctggg
2401 cagccggggg gtgaagctgc tctgtcaagg actcagacac cccaactgca aacttcagaa
2461 cctgaggctg aagaggtgcc gcatctccag ctcagcctgc gaggacctct ctgcagctct
2521 catagccaat aagaatttga caagatgga tctcagtggc aacggcggtg gattcccagg
2581 catgatgctg ctttgcgagc gcctgcggca tcccagtgct aggctgcaga tgattcagtt
2641 gaggaagtgt cagctggagt ccggggcctt tcaggagatg gcttctgtgc tgggcaccaa
2701 cccacatctg gttgagttgg acctgacagg aaatgcactg gaggatttgg gcctgaggtt
```

```
2761 actatgccag ggactgaggc acccagtctg cagactacgg actttgtggc tgtggctgga
2821 tagctgtggc ctcacagcca aggcttgtga gaatctttac ttcaccctgg ggatcaacca
2881 gaccttgacc gacctttacc tgaccaacaa cgccctaggg gacacaggtg tccgactgct
2941 ttgcaagcgg ctgagccatc ctgggtgcaa actccgagtc ctctggttat ttgggatgga
3001 cctgaataaa atgaccacaca gtaggttggc agcgcttcga gtaacaaaac cttatttgga
3061 cattggctgc tgaatggtcc tatctgctgg ctctcccctg agatctggac agaggaagat
3121 gggaggggtgc tcatcacccc cccagcataa tgatcagcct ccttcctaga gacagactca
3181 tgcagattga gatcaaaagt ccctctgctt gggatcaaataaatggtttga cagagctggc
3241 caggcgtggt ggctcatgta tgtaatccta gcacttcgag aggccgaggc aggtggatca
3301 cgaggtcagg agtttgagat tagcctggcc aagatggtga aaccctgtct ctactaaaaa
3361 taaaaaaaaa ttagccagga aaaaaaaaaa aaaaa
```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42




My NCBI
[\[Sign In\]](#)
[\[Register\]](#)

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search ☒ for

Limits Preview/Index History Clipboard Details

Display ☒ Show ☒ Send to ☒

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒
☐ 1: [AY116207](#). Reports Homo sapiens mona...[gi:21711826]

[Links](#)

LOCUS AY116207 3221 bp mRNA linear PRI 21-MAY-2003

DEFINITION Homo sapiens monarch-1 splice form IV mRNA, complete cds; alternatively spliced.

ACCESSION AY116207

VERSION AY116207.1 GI:21711826

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3221)

AUTHORS Williams, K.L., Taxman, D.J., Linhoff, M.W., Reed, W. and Ting, J.P.Y.

TITLE Monarch-1: A Pyrin/Nucleotide-Binding Domain/Leucine-Rich Repeat Protein That Controls Classical and Nonclassical MHC Class I Genes

JOURNAL J. Immunol. 170 (11), 5354-5358 (2003)

PUBMED 12759408

REFERENCE 2 (bases 1 to 3221)

AUTHORS Williams, K.L., Linhoff, M.W. and Ting, J.P.Y.

TITLE Direct Submission

JOURNAL Submitted (29-MAY-2002) Lineberger Cancer Center, UNC, Mason Farm Road, Chapel Hill, NC 27599, USA

FEATURES Location/Qualifiers

source 1..3221
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="19"
/map="19q13.4"

CDS 221..2899
/note="contains alternatively spliced exons 7, 8 and 9"
/codon_start=1
/product="monarch-1 splice form IV"
/protein_id="AAM75145.1"
/db_xref="GI:21711827"

/translation="MLRTAGRDGLCRLSTYLEELEAVELKKFKLYLGTATELGEGKIP
WGSMEKAGPLEMAQLLITHFGPEAWRLALSTFERINRKDLWERGQREDLVRDTPPGG
PSSLGNQSTCLLEVSLVTPRKDPQETYRDYVRRKFRLMEDRNARLGECVNLSHRYTRL
LLVKEHSNPMQVQQQLLDTGRGHARTVGHQASPIKIETLFEPDEERPEPPRTVVMQGA
AGIGKSMLAHKVMLDWADGKLFQGRFDYLFYINCREMNSATECSMQDLIFSCWPEPS
APLQELIRVPERLLFIIDGFDELKPSFHDPQGPWCWCWEEKRPTELLNSLIRKKLLP
ELSLITTRPTALEKLHRLLEHPRHVEILGFSEAERKEYFYKYFHNAEQAGQVFNVVR
DNEPLFTMCFVPLVCVVCTCLQQQLEGGLLRQTSRTTTAVYMLYLLSLMQPKPGAP
RLQPPPNQRGLCSLAADGLWNQKILFEEQDLRKHGLDGEDVSAFLNMNIFQKDINCR
YYSFIHLSFQEFFAAMYIILDEGEGGAGPDQDVTRLLTEYAFSERSFLALTSRFLFGL"

LNEETRSHLEKSLCWKVSPHIKMDLLQWIQSKAQSDGSTLQQGSLEFFSCLYEIQEEE
FIQQALSHFQVIVVSNIAKMEHVMSSFCLKRCRSAQVLHLYGATYSADGEDRARC
GAHTLLVQLRPERTVLLDAYSEHLAAALCTNPNIELSLYRNALGSRGVKLLCQGLRH
PNCKLQNLRLKRCRISSSACEDLSAALIANKNLTRMDLSGNGVGFPGMMLLCEGLRHP
QCRLQMIQLRKQLESGACQEMASVLGTNPHLVELDLTGNALEDLGLRLLCQGLRHPV
CRLRTLWWLFGMDLNKMTSRLAALRVTKPYLDIGC"

misc feature 869..892

/note="Region: P-loop"

misc feature 2069..2896

/note="Region: leucine rich repeat"

misc feature 221..289

/note="Region: pyrin domain"

ORIGIN

```
1 attggtgagt ggggcagggc aggaggggaac tgaagagtga gaaagcatta tttcagcaaa
61 aggtctttcc tcccttgctc actcctccaa ccactggctc agcctctccg cccgctgcct
121 gtgaatgatg caatggaagg tgtgctgggg tcgccctgtg tcccgtgcat aggagcatct
181 cagcctccag gtcctctcct ttggggctta cggcaccccc atgctacgaa ccgcaggcag
241 ggacggcctc tgtcgctgtt ccacctactt ggaagaactc gaggctgtgg aactgaagaa
301 gttcaagtta tacctgggga ccgcgacaga gctgggagaa ggcaagatcc cctggggaag
361 catggagaag gccggtcccc tggaaatggc ccagctgctc atcaccactc tcggggccaga
421 ggaggcctgg aggttggctc tcagcacctt tgagcggata aacaggaagg acctgtggga
481 gagaggacag agagaggacc tggtagggga taccacactt ggtggcccgt cctcacttgg
541 gaaccagtca acatgccttc tggaaagtctc tcttgtcact ccaagaaaag atccccagga
601 aacctacagg gactatgtcc gcaggaaatt ccggctcatg gaagaccgca atgcgcgcct
661 aggggaatgt gtcaacctca gccaccggta caccggctc ctgctggtga aggagcactc
721 aaaccccatg caggtccagc agcagcttct ggacacaggc cggggacacg cgaggaccgt
781 gggacaccag gctagcccca tcaagataga gaccctcttt gagccagacg aggagcgccc
841 cgagccaccg cgcaccgtgg tcatgcaagg cgcggcaggg ataggcaagt ccatgctggc
901 acacaagggtg atgctggact gggcggacgg gaagctcttc caaggcagat ttgattatct
961 cttctacatc aactgcaggg agatgaacca gagtgccacg gaatgcagca tgcaagacct
1021 catcttcagc tgctggcctg agcccagcgc gcctctccag gagctcatcc gagttcccga
1081 gcgcctcctt ttcattcatc acggcttcga tgagctcaag ccttctttcc acgatcctca
1141 gggaccctgg tgctctgctt gggaggagaa acggcccacg gagctgcttc ttaacagctt
1201 aattcggaag aagctgctcc ctgagctatc tttgctcatc accacacggc ccacggcttt
1261 ggagaagctc caccgtctgc tggagcacc caggcatgtg gagatcctgg gcttctctga
1321 ggcagaaagg aaggaatact tctacaagta tttccacaat gcagagcagg cgggccaagt
1381 cttcaattac gtgagggaca acgagcctct cttaccatg tgcttcgtcc ccttggtgtg
1441 ctgggtggtg tgtacctgcc tccagcagca ctgggagggt ggggggctgt tgagacagac
1501 gtccaggacc accactgcag tgtacatgct ctacctgctg agtctgatgc aacccaagcc
1561 gggggccccc cgctccagc cccaccccaa ccagagaggg ttgtgctcct tggcggcaga
1621 tgggctctgg aatcagaaaa tcctatttga ggagcaggac ctccggaagc acggcctaga
1681 cggggaagac gtctctgcct tcctcaacat gaacatcttc cagaaggaca tcaactgtga
1741 gaggtactac agcttcatcc acttgagttt ccaggaattc tttgcagcta tgtactatat
1801 cctggacgag ggggagggcg gggcaggccc agaccaggac gtgaccaggc tgttgaccga
1861 gtacgcgttt tctgaaagga gcttcttggc actcaccagc cgcttctgtt ttggactcct
1921 gaacgaggag accaggagcc acctggagaa gagtctctgc tgggaaggtct cgccgcacat
1981 caagatggac ctggttgcat ggatccaaag caaagctcag agcgacggct ccaccctgca
2041 gcagggctcc ttggagtctt tcagctgctt gtacgagatc caggaggagg agtttatcca
2101 gcaggccctg agccacttcc aggtgatcgt ggtcagcaac attgcctcca agatggagca
2161 catggtctcc tcgttctgtc tgaagcgctg caggagcgcc caggtgctgc acttgatagg
2221 cgccacctac agcgcgagcg ggaagaccg cgcgaggtgc tccgcaggag cgcacacgct
2281 gttggtgcag ctgagaccag agaggaccgt tctgctggac gcctacagtg aacatctggc
2341 agcgccctg tgcaaccaatc caaacctgat agagctgtct ctgtaccgaa atgccctggg
2401 cagccggggg gtgaagctgc tctgtcaagg actcagacac cccaactgca aacttcagaa
2461 cctgaggctg aagaggtgcc gcatctccag ctgagcctgc gaggacctct ctgcagctct
2521 catagccaat aagaatttga caaggatgga tctcagtggc aacggcgctt gattcccagg
2581 catgatgctg ctttgcgagg gcctgcggca tccccagtgc aggtgcaga tgattcagtt
2641 gaggaagtgt cagctggagt ccggggcttg tcaggagatg gcttctgtgc tcggcaccaa
2701 cccacatctg gttgagttgg acctgacagg aatgcactg gaggatttgg gcctgaggtt
2761 actatgccag ggactgaggc acccagctctg cagactacgg actttgtggg ggttatttgg
```

2821 gatggacctg aataaaatga cccacagtag gttggcagcg cttcgagtaa caaacctta
2881 tttggacatt ggctgctgaa tggtcctatc tgctggctct cccctgagat ctggacagag
2941 gaagatggga ggggtgctcat cccccccca gcataatgat cagcctcctt cctagagaca
3001 gactcatgca gattgagatc aaaagtcctt ctgcttggga tcaaattaat gtttgacaga
3061 gctggccagg cgtgggtggct catgtatgta atcctagcac ttcgagaggc cgaggcaggt
3121 ggatcacgag gtcaggagtt tgagattagc ctggccaaga tggtgaaacc ctgtctctac
3181 taaaaataaa aaaaaattag ccaggaaaaa aaaaaaaaaa a

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42




[\[Sign In\]](#)
[\[Register\]](#)

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search ☒ for

Limits Preview/Index History Clipboard Details

Display **GenBank** Show **5** Send to

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

1: [AY154469](#). Reports Homo sapiens NALP...[gi:28436381] [Links](#)

LOCUS	AY154469	3282 bp	mRNA	linear	PRI 20-FEB-2003
-------	----------	---------	------	--------	-----------------

DEFINITION Homo sapiens NALP14 (NALP14) mRNA, complete cds.

ACCESSION AY154469

VERSION AY154469.1 GI:28436381

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 3282)

AUTHORS Tschopp, J., Martinon, F. and Burns, K.

TITLE NALPs: a novel protein family involved in inflammation

JOURNAL Nat. Rev. Mol. Cell Biol. 4 (2), 95-104 (2003)

PUBMED 12563287

REFERENCE 2 (bases 1 to 3282)

AUTHORS Martinon, F., Hofmann, K. and Tschopp, J.

TITLE Direct Submission

JOURNAL Submitted (25-SEP-2002) Institute of Biochemistry, University of
Lausanne, ch. des Boveresses 155, Epalinges, VD 1066, Switzerland

FEATURES	Location/Qualifiers
----------	---------------------

```
source      1..3282
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
```

```
gene      1..3282
          /gene="NALP14"
```

CDS

```
1..3282
/gene="NALP14"
/note="member of the NALP protein family involved in
inflammation; contains NACHT, LRR and PYD domains"
/codon_start=1
/product="NALP14"
/protein_id="AA018165.1"
/db xref="GI:28436382"
```

```
/translation="MADSSSSFFPDFGLLLYLEELNKEELNTFKLFLKETMEPEHGL
TPWNEVKKARREDLANLMKKYYPGEKAWSVSLKIFGKMNLDKLCERAKEEINWSAQTI
GPDDAKAGETQEDQEAVLGDGTEYRNRIKEKFCITWDKKS LAGKPEDFHHGIAEKDRK
LLEHLFDVDVKTGAQPQIVVLQGAAGVGKTTLVRKAMDWAEGSLYQQRKFYVFYLNQ
REINQLKERSFAQLISKDWPSTEGPIEEIMYQPSSLLFIIDSFDELNF AFEEPEFALC
EDWTQEHVPSFLMSSLLRKVMLPEASLLVTTTRLTTSKRLKQLLKNHHYVELLGMSEDA
REEYIYQFFEDKRWAMKVFSSLSNEMLFSCMQVPLVCWAACCTCLKQQMEKGGDVTLT
CQTTTALFTCYISSLFTPDVGGSPLPNQAQLRRLCQVAAKGIWMTYVFYRENLRRL
GLTQSDVSSFMDSNIIQKDAEYENCYVFTLHVQEFFAAMFYMLKGSWEAGNPSCQPF
EDLKSLLQSTSYKDPHLTQMKCFLGLLNEDRVKOLERTFNCKMSLKI KSKLLOCMEV
```


LGNSDYSPSQLGFLELFHCLYETQDKAFISQAMRCFPKVAINICEKIHLVSSFCCLKH
 CRCLRTIRLSVTTVFEEKILKTSLPTNTWDGDRITHCWQDLCSVLHTNEHLRELDLYH
 SNLDKSAMNIIHHELRHPNCKLQKLLKLFITFPDGCQDISTSIIHNKNLMHLDLKGSD
 IGDNGVKSLEALKHPECKLQTLRLSCNLTVFCCLNISNALIRSQSLIFLNLSTNNL
 LDDGVQLLCEALRHPKCYLERLSLESCGLTEAGCEYLSLALISNKRLTHLCLADNVLG
 DGGVKLMSDALQHAQCTLKSLVLRCHFTSLSSSEYLSLSTLLHNKSLTHLDLGSNWLDQD
 NGVKLLCDVFRHPSCNLQDLELMGCVLTNACCLDLASVILNNPNLRSLLDLGNNDLQDD
 GVKILCDALRYPNICNIQRLGLECYGLTSLCCQDLSSALICNKRLIKMNLTONTLGYEG
 IVKLYKVLKSPKCKLQVLGLCKEAFDEEAQKLEAVGVSNPHLIIKPDCNYHNEEDVS
 WWWCF"

ORIGIN

```

1 atggcagatt catcatcatc ttctttcttt cctgattttg ggctgctatt gtatttgag
61 gagctaaaca aagaggaatt aaatacattc aagttattcc taaaggagac catggaacct
121 gagcatggcc tgacaccctg gaatgaagtg aagaaggcca ggcgggagga cctggccaat
181 ttgatgaaga aatattatcc aggagagaaa gcctggagtg tgtctctcaa aatctttggc
241 aagatgaacc tgaaggatct gtgtgagaga gcgaaagaag agatcaactg gtcggcccag
301 actataggac cagatgatgc caaggctgga gagacacaag aagatcagga ggcagtgctg
361 ggtgatggaa cagaatacag aaatagaata aaggaaaaat tttgcatcac ttgggacaag
421 aagtcttttg ctggaaagcc tgaagatttc catcatggaa ttgcagagaa agatagaaaa
481 ctggttgaac acttgttcga tgtggatgtc aaaaccggtg cacagccaca gatcgtggtg
541 cttcagggag ctgctggagt tgggaaaaca accttggtga gaaaggcaat gttagattgg
601 gcagagggca gtctctacca gcagaggttt aagtatgttt tttatctcaa tgggagagaa
661 attaaccagc tgaaagagag aagctttgct caattgatat caaaggactg gcccagcaca
721 gaaggcccca ttgaagaaat catgtaccag ccaagtagcc tcttgtttat tattgacagt
781 ttcgatgaac tgaactttgc ctttgaagaa cctgagtttg cactgtgcga agactggacc
841 caagaacacc cagtgtcctt cctcatgagt agtttgctga ggaaagtgat gctccctgag
901 gcatccttat tggtgacaac aagactcaca acttctaaga gactaaagca gttgttgaag
961 aatcaccatt atgtagagct actaggaatg tctgaggatg caagagagga gtatatttac
1021 cagttttttg aagataagag gtggggccatg aaagtattca gttcactaaa aagcaatgag
1081 atgctgttta gcatgtgcc agtcccccta gtgtgctggg ccgcttgtag ttgtctgaag
1141 cagcaaatgg agaagggtgg tgatgtcaca ttgacctgcc aaacaaccac agctctgttt
1201 acctgctata tttctagctt gttcacacca gtagatggag gctctcctag tctacccaac
1261 caagcccagc tgagaagact gtgccaagtc gctgccaaag gaatatggac tatgacttac
1321 gtgtttttaca gagaaaatct cagaaggctt ggggttaactc aatctgatgt ctctagtttt
1381 atggacagca atattattca gaaggacgca gtagatgaaa actgctatgt gttcaccac
1441 cttcatgttc aggagttttt tgcagctatg ttctatatgt tgaaaggcag ttgggaagct
1501 gggaaacctt cctgccagcc ttttgaagat ttgaagtcac tacttcaaag cacaagttat
1561 aaagaccccc atttgacaca gatgaagtgc tttttgttg gccttttgaa tgaagatcga
1621 gtaaaacaac tggagaggac tttaaactgt aaaatgtcac tgaagataaa atcaaagttta
1681 cttcagtgtg tggaaagtatt aggaaacagt gactattctc catcacagct gggatttctg
1741 gagttgtttc actgtctgta tgagactcaa gataaagcgt ttataagcca gggcaatgaga
1801 tgtttcccaa aggttgccat taatatttgt gagaaaatac atttgcttgt atcttctttc
1861 tgccttaagc actgccggtg tttgcggacc atcaggctgt ctgtaactgt ggtatttgag
1921 aagaagatat taaaaacaag cctcccaact aacacttggg atggtgatcg cattactcac
1981 tgttggaag atctctgttc tgtgcttcat acaaatgaac acttgagaga attggacctg
2041 taccatagca accttgataa atcagcaatg aatatcctgc atcatgaact aaggcaccac
2101 aactgtaaac tacaaaagct actgttgaaa tttatcactt tccctgatgg ttgtcaggat
2161 atctctactt ctttgattca taacaagaat ctgatgcatc ttgacctaaa agggagtgat
2221 ataggggata atggagtaaa gtcatttgtg gaggccttga aacaccagga gtgtaaacta
2281 cagactctca ggctggaatc ttgcaacctt actgtatttt gttgtctaaa tatatcta
2341 gctctcatca gaagccagag cctgatattt ctgaatctgt caaccaataa tctgttggat
2401 gatggagtgc agctttttgt tgaggcctta agacatccaa agtgttatct agagagactg
2461 tccttagaaa gctgtggtct cacagaggct ggctgtgagt atctttcttt ggctctcatc
2521 agcaataaaa gactgacaca tttgtgcttg gcagacaatg tcttgggtga tgggtggagta
2581 aagcttatga gtgatgccct gcaacatgca caatgtactc tgaagagcct tgtgctgagg
2641 cgttgccatt tcacttcact tagcagtga tatctgtcaa cttctcttct acacaacaag
2701 agcctgacgc atctggatct aggatcaaac tggctacaag acaatggagt gaagcttctg
2761 tgtctgtctc ttggcatcc aagctgtaat cttcaggact tgggaattgat gggctgtgtt
2821 ctactaatg catgttgtct ggatctggct tctgttattt tgaataacct aaacctgagg
2881 agcctggacc ttgggaacaa cgatttgtag gatgatggag tgaaaattct gtgtgatgct

```

2941 ttgagatatc caaactgtaa cattcagagg ctcggttg aatactgtgg tttgacatct
3001 ctctgctgtc aagatctctc ctctgctctt atctgcaaca aaagactgat aaaaatgaat
3061 ctgacacaga ataccttagg atatgaagga attgtgaagt tatataaagt cttgaagtct
3121 cctaagtgtg aactacaagt tctaggggtg tgcaaagagg catttgatga ggaagcccag
3181 aagctgctgg aagctgtggg agttagcaat ccacacttaa tcattaagcc agattgtaac
3241 tatcataatg aagaagatgt gtcttggtgg tgggtgttct ga

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42




[\[Sign In\]](#)
[\[Register\]](#)

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Limits Preview/Index History Clipboard Details

Display **GenBank**  Show **5**  Send to 

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [BC013199](#). Reports Homo sapiens NOD9...[gi:16753263] [Links](#)

LOCUS	BC013199	2177 bp	mRNA	linear	PRI 27-APR-2005
-------	----------	---------	------	--------	-----------------

DEFINITION Homo sapiens NOD9 protein, mRNA (cDNA clone IMAGE:4387619), partial cds.

ACCESSION BC013199

VERSION BC013199.1 GI:16753263

KEYWORDS

SOURCE	Homo sapiens (human)
--------	----------------------

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 2177)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H.; Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

CONSRTM Mammalian Gene Collection Program Team

TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
-------	--

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932

REFERENCE 2 (bases 1 to 2177)

AUTHORS
CONSRTM NIH MGC Project

TITLE Direct Submission

JOURNAL Submitted (27-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hqsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 26 Row: p Column: 19.

FEATURES

source	Location/Qualifiers
	1..2177
	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="IMAGE:4387619"
	/tissue_type="Bone, osteosarcoma"
	/clone_lib="NIH_MGC_86"
	/lab_host="DH10B"
	/note="Vector: pCMV-SPORT6"
gene	<1..2177
	/gene="NOD9"
	/note="synonyms: FLJ21478, MGC21025"
	/db_xref="GeneID:79671"
CDS	<1..2127
	/gene="NOD9"
	/codon_start=1
	/product="NOD9 protein"
	/protein_id="AAH13199.3"
	/db_xref="GI:62913995"
	/db_xref="GeneID:79671"
	/translation="QLVAQRYTPLKEVLPLMAAAGSHLLFVLHGLEHLNLDFRLAGTG LCSDPEEPQEPAAIIVNLLRKYMLPQASILVTTTPSAIGRIPSKYVGRYGEICGFSDT NLQKLYFQLRLNQPYCGYAVGGSGVSATPAQRDHLVQMLSRNLEGGHQAIAACFLPSY CWLVCATLHFLHAPTAPAGQTLTSIYTSFLRLNFSGETLDSTDPSNLSLMAYAARTMGK LAYEGVSSRKTYFSEEDVCGCLEAGIRTEEEFQLLHIFRRDALRFFLAPCPEPGRAGT FVFTVPAMQEYLAALYIVLGLRKTTLQKVGKEVAELVGRVGEDVSLVLGIMAKLLPLR ALPLLFNLIKVVPVFRMVGKSREAVAQAMVLEMFREEDYNDVDVLDQMGASILGVE GPRRHPDEPPPEDEVFELFPMFMGGLLSAHNRAVLAQLGCPIKNLDALENAQAIAKKKLG KLGRQVLPPSELDDLHFFHYEFQNRFSAEVLSSLRQLNLGAVRMTVPVKCTVVAVLG SGRHALDEVNLASCQLDPAGLRTLLPVFLRARKLGLQLNSLGPEACKDLRDLHLDQC QITTLRLSNNPLTEAGVAVLMEGLAGNTSVTHLSLLHTGLGDEGLELLAAQLDRNRQL QELNVAYNGAGDTAALALARAAREHPSLELLQGVAIQMCWKPLLPYAHLWTPRMPSH WCFLLILMPPLPQWYDGLVAPRGRC"
misc difference	1739
	/gene="NOD9"
	/note="'A' in cDNA is 'C' in the human genome; amino acid difference: 'E' in cDNA, 'A' in the human genome. The chimpanzee genome agrees with the human genomic sequence and not the cDNA; Differences found between this sequence and the human reference genome (build 35) are described in misc_difference features below and these differences were also compared to chimpanzee genomic sequences available as of 09/15/2004 00:00:00"
misc difference	2164..2177
	/gene="NOD9"

/note="polyA tail: 14 bases do not align to the human genome; Differences found between this sequence and the human reference genome (build 35) are described in misc_difference features below and these differences were also compared to chimpanzee genomic sequences available as of 09/15/2004 00:00:00"

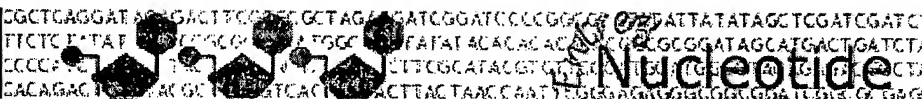

ORIGIN

```
1 caacttgtgg cccagcgcta cacgcccctg aaggagggttc tgcccctgat ggctgctgct
61 ggggtcccacc tcctctttgt gctccatggc ttagagcatc tcaacctcga cttccggctg
121 gcaggcacgg gactttgtag tgaccgggag gaaccgcagg aaccagctgc tatcatcgct
181 aacctgctgc gcaaatacat gctgcctcag gccagcattc tggtgaccac tcggccctct
241 gccattggcc gtatccccag caagtacgtg ggccgctatg gtgagatctg cggtttctct
301 gataccaacc tgcagaagct ctacttcag ctccgcctca accagccgta ctgcgggtat
361 gccgttggcg gttcaggtgt ctctgccaca ccagctcagc gtgaccacct ggtgcagatg
421 ctctcccgga acctggaggg gcaccaccag atagccgctg cctgcttctt gccgtcttat
481 tgctggctcg tttgtgccac cttgcacttc ctgcatgccc ccacgcctgc tgggcagacc
541 cttacaagca tctataccag cttcctgcgc ctcaacttca gcggggaaac cctggacagc
601 actgaccctt ccaatttgtc cctgatggcc tatgcagccc gaaccatggg caagtggcc
661 tatgaggggg tgctctcccg caagacctac ttctctgaag aggatgtctg tgggtgctg
721 gaggttgcca tcaggacgga ggaggagttt cagctgctgc acatcttccg tcgggatgcc
781 ctgaggtttt tcctggcccc atgtgtggag ccaggggctg caggcacctt cgtgttcacc
841 gtgcccgcga tgcaggaata cctggctgcc ctctacattg tgctgggttt gcgcaagacg
901 accctgcaaa aggtgggcaa ggaagtggct gagctcgtgg gccgtgttgg ggaggacgtc
961 agcctggtac tgggcatcat ggccaagctg ctgcctctgc gggctctgcc tctgctcttc
1021 aacctgatca aggtggttcc acgagtgttt gggcgcatgg tgggtaaaag ccgggaggcg
1081 gtggctcagg ccatggtgct ggagatgttt cgagaggagg actactaaa cgatgatgtt
1141 ctggaccaga tgggcgccag tatcctgggc gtggaggggc cccggcgcca cccagatgag
1201 cccctgagg atgaagtctt cgagctcttc cccatgttca tgggggggct tctctctgcc
1261 cacaaccgag ctgtgctagc tcagcttggc tgcccatca agaacctgga tgccctggag
1321 aatgcccagg ccatcaagaa gaagctgggc aagctgggcc ggcaggtgct gccccatca
1381 gagtccttg accacctctt cttccactat gagttccaga accagcgctt ctccgctgag
1441 gtgctcagct ccctgcgtca gctcaacctg gcaggtgtgc gcatgacacc agtcaagtgc
1501 acagtggtag cagctgtgct gggcagcgga aggcagctgc tggatgaggt gaacttggcc
1561 tcctgccagc tagatcctgc tgggtgcgc aactcctgc ctgtcttctt gcgtgcccg
1621 aagctgggct tgcaactcaa cagcctgggc cctgaggcct gcaaggacct ccgagacctg
1681 ttgctgcatg accagtcca aattaccaca ctgcggctgt ccaacaacc gctgacggag
1741 gcaggtgttg ccgtgcta at ggaggggctg gcaggaaaca cctcagtga cgcacctgtc
1801 ctgctgcaca cgggccttgg ggacgaaggc ctggagctgc tggctgccc gctggaccgc
1861 aaccggcagc tgcaggagct gaacgtggcg tacaacggtg ctggtgacac agcggccctg
1921 gccctggcca gagctgcccg ggagaccct tccctggaac tgctacagg tgctgccatc
1981 cagatgtgtt ggaagcttcc cctcctgcct tatgctcacc tgtggacacc gaggatgcc
2041 tcacattggt gctttctcct catcctcatg cccctttgc cacaatggtg tgatggcttg
2101 gtagccctc gaggcagatg cacctgactt gctgctatta aaaagccgtg tgccttctac
2161 caaaaaaaaa aaaaaaa
```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42



My NCBI
[Sign In](#)
[Register](#)

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for Display 5 Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒☐ 1: [NM_004895](#). Reports Homo sapiens cold...[gi:34878692][Links](#)

LOCUS NM_004895 4484 bp mRNA linear PRI 17-OCT-2005

DEFINITION Homo sapiens cold autoinflammatory syndrome 1 (CIAS1), transcript variant 1, mRNA.

ACCESSION NM_004895

VERSION NM_004895.3 GI:34878692

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4484)

AUTHORS Arostegui,J.I., Aldea,A., Modesto,C., Rua,M.J., Arguelles,F., Gonzalez-Ensenat,M.A., Ramos,E., Rius,J., Plaza,S., Vives,J. and Yague,J.

TITLE Clinical and genetic heterogeneity among Spanish patients with recurrent autoinflammatory syndromes associated with the CIAS1/PYPAF1/NALP3 gene

JOURNAL Arthritis Rheum. 50 (12), 4045-4050 (2004)

PUBMED [15593220](#)

REMARK GeneRIF: Missense mutations of CIAS1/PYPAF1/NALP3 gene occurred in 7 unrelated Spanish families with recurrent autoinflammatory diseases.

REFERENCE 2 (bases 1 to 4484)

AUTHORS Dowds,T.A., Masumoto,J., Zhu,L., Inohara,N. and Nunez,G.

TITLE Cryopyrin-induced interleukin 1beta secretion in monocytic cells: enhanced activity of disease-associated mutants and requirement for ASC

JOURNAL J. Biol. Chem. 279 (21), 21924-21928 (2004)

PUBMED [15020601](#)

REMARK GeneRIF: cryopyrin disease-associated mutants are constitutively active and able to induce NF-kappaB activation and IL-1beta secretion at least in part by an increased ability to interact with ASC

REFERENCE 3 (bases 1 to 4484)

AUTHORS Neven,B., Callebaut,I., Prieur,A.M., Feldmann,J., Bodemer,C., Lepore,L., Derfalvi,B., Benjaponpitak,S., Vesely,R., Sauvain,M.J., Oertle,S., Allen,R., Morgan,G., Borkhardt,A., Hill,C., Gardner-Medwin,J., Fischer,A. and de Saint Basile,G.

TITLE Molecular basis of the spectral expression of CIAS1 mutations associated with phagocytic cell-mediated autoinflammatory disorders CINCA/NOMID, MWS, and FCU

JOURNAL Blood 103 (7), 2809-2815 (2004)

PUBMED [14630794](#)

REMARK GeneRIF: mutated in CINCA syndrome

- REFERENCE 4 (bases 1 to 4484)
AUTHORS Agostini,L., Martinon,F., Burns,K., McDermott,M.F., Hawkins,P.N. and Tschoop,J.
TITLE NALP3 forms an IL-1beta-processing inflammasome with increased activity in Muckle-Wells autoinflammatory disorder
JOURNAL Immunity 20 (3), 319-325 (2004)
PUBMED [15030775](#)
REMARK GeneRIF: NALP3 forms a protein complex that processes IL-1 beta in macrophages from a patient with the Muckle-Wells autoinflammatory disorder.
- REFERENCE 5 (bases 1 to 4484)
AUTHORS O'Connor,W. Jr., Harton,J.A., Zhu,X., Linhoff,M.W. and Ting,J.P.
TITLE Cutting edge: CIAS1/cryopyrin/PYPAF1/NALP3/CATERPILLER 1.1 is an inducible inflammatory mediator with NF-kappa B suppressive properties
JOURNAL J. Immunol. 171 (12), 6329-6333 (2003)
PUBMED [14662828](#)
REMARK GeneRIF: CIAS1/cryopyrin may act as a key regulator of inflammation, induced to dampen NF-kappa B-dependent proinflammatory signals.
- REFERENCE 6 (bases 1 to 4484)
AUTHORS Dowds,T.A., Masumoto,J., Chen,F.F., Ogura,Y., Inohara,N. and Nunez,G.
TITLE Regulation of cryopyrin/Pypaf1 signaling by pyrin, the familial Mediterranean fever gene product
JOURNAL Biochem. Biophys. Res. Commun. 302 (3), 575-580 (2003)
PUBMED [12615073](#)
REMARK GeneRIF: there is a cryopyrin signaling pathway activated through the induced proximity of ASC, which is negatively regulated by pyrin
- REFERENCE 7 (bases 1 to 4484)
AUTHORS Tschoop,J., Martinon,F. and Burns,K.
TITLE NALPs: a novel protein family involved in inflammation
JOURNAL Nat. Rev. Mol. Cell Biol. 4 (2), 95-104 (2003)
PUBMED [12563287](#)
REMARK Review article
- REFERENCE 8 (bases 1 to 4484)
AUTHORS Hoffman,H.M., Gregory,S.G., Mueller,J.L., Tresieras,M., Broide,D.H., Wanderer,A.A. and Kolodner,R.D.
TITLE Fine structure mapping of CIAS1: identification of an ancestral haplotype and a common FCAS mutation, L353P
JOURNAL Hum. Genet. 112 (2), 209-216 (2003)
PUBMED [12522564](#)
REMARK GeneRIF: a single heterozygous missense mutation (T1058C=L353P) in exon 3 of CIAS1 in all four families that is responsible for the large majority of FCAS cases
- REFERENCE 9 (bases 1 to 4484)
AUTHORS Granel,B., Philip,N., Serratrice,J., Ene,N., Grateau,G., Dode,C., Cuisset,L., Disdier,P., Berbis,P., Delpech,M. and Weiller,P.J.
TITLE CIAS1 mutation in a patient with overlap between Muckle-Wells and chronic infantile neurological cutaneous and articular syndromes
JOURNAL Dermatology (Basel) 206 (3), 257-259 (2003)
PUBMED [12673085](#)
- REFERENCE 10 (bases 1 to 4484)
AUTHORS Aksentijevich,I., Nowak,M., Mallah,M., Chae,J.J., Watford,W.T., Hofmann,S.R., Stein,L., Russo,R., Goldsmith,D., Dent,P., Rosenberg,H.F., Austin,F., Remmers,E.F., Balow,J.E. Jr., Rosenzweig,S., Komarow,H., Shoham,N.G., Wood,G., Jones,J., Mangra,N., Carrero,H., Adams,B.S., Moore,T.L., Schikler,K., Hoffman,H., Lovell,D.J., Lipnick,R., Barron,K., O'Shea,J.J.,

TITLE Kastner,D.L. and Goldbach-Mansky,R.
 De novo CIAS1 mutations, cytokine activation, and evidence for genetic heterogeneity in patients with neonatal-onset multisystem inflammatory disease (NOMID): a new member of the expanding family of pyrin-associated autoinflammatory diseases
 JOURNAL Arthritis Rheum. 46 (12), 3340-3348 (2002)
 PUBMED [12483741](#)
 REMARK GeneRIF: De novo CIAS1 mutations in neonatal-onset multisystem inflammatory disease. We found 6 heterozygous missense substitutions in CIAS1. Germline mutations.
 REFERENCE 11 (bases 1 to 4484)
 AUTHORS Fiorentino,L., Stehlik,C., Oliveira,V., Ariza,M.E., Godzik,A. and Reed,J.C.
 TITLE A novel PAAD-containing protein that modulates NF-kappa B induction by cytokines tumor necrosis factor-alpha and interleukin-1beta
 JOURNAL J. Biol. Chem. 277 (38), 35333-35340 (2002)
 PUBMED [12093792](#)
 REFERENCE 12 (bases 1 to 4484)
 AUTHORS Aganna,E., Martinon,F., Hawkins,P.N., Ross,J.B., Swan,D.C., Booth,D.R., Lachmann,H.J., Bybee,A., Gaudet,R., Woo,P., Feighery,C., Cotter,F.E., Thome,M., Hitman,G.A., Tschopp,J. and McDermott,M.F.
 TITLE Association of mutations in the NALP3/CIAS1/PYPAF1 gene with a broad phenotype including recurrent fever, cold sensitivity, sensorineural deafness, and AA amyloidosis
 JOURNAL Arthritis Rheum. 46 (9), 2445-2452 (2002)
 PUBMED [12355493](#)
 REMARK GeneRIF: Mutations in the NALP3/CIAS1/PYPAF1 gene are associated with familial cold urticaria and Muckle-Wells syndrome.
 REFERENCE 13 (bases 1 to 4484)
 AUTHORS Feldmann,J., Prieur,A.M., Quartier,P., Berquin,P., Certain,S., Cortis,E., Teillac-Hamel,D., Fischer,A. and de Saint Basile,G.
 TITLE Chronic infantile neurological cutaneous and articular syndrome is caused by mutations in CIAS1, a gene highly expressed in polymorphonuclear cells and chondrocytes
 JOURNAL Am. J. Hum. Genet. 71 (1), 198-203 (2002)
 PUBMED [12032915](#)
 REMARK GeneRIF: Chronic infantile neurological cutaneous and articular syndrome is caused by mutations in CIAS1, a gene highly expressed in polymorphonuclear cells and chondrocytes.
 REFERENCE 14 (bases 1 to 4484)
 AUTHORS Srinivasula,S.M., Poyet,J.L., Razmara,M., Datta,P., Zhang,Z. and Alnemri,E.S.
 TITLE The PYRIN-CARD protein ASC is an activating adaptor for caspase-1
 JOURNAL J. Biol. Chem. 277 (24), 21119-21122 (2002)
 PUBMED [11967258](#)
 REFERENCE 15 (bases 1 to 4484)
 AUTHORS Dode,C., Le Du,N., Cuisset,L., Letourneur,F., Berthelot,J.M., Vaudour,G., Meyrier,A., Watts,R.A., Scott,D.G., Nicholls,A., Granel,B., Frances,C., Garcier,F., Edery,P., Boulinguez,S., Domergues,J.P., Delpech,M. and Grateau,G.
 TITLE New mutations of CIAS1 that are responsible for Muckle-Wells syndrome and familial cold urticaria: a novel mutation underlies both syndromes
 JOURNAL Am. J. Hum. Genet. 70 (6), 1498-1506 (2002)
 PUBMED [11992256](#)
 REMARK GeneRIF: New mutations of CIAS1 that are responsible for Muckle-Wells syndrome and familial cold urticaria: a novel mutation underlies both syndromes.
 REFERENCE 16 (bases 1 to 4484)

AUTHORS Manji,G.A., Wang,L., Geddes,B.J., Brown,M., Merriam,S.,
Al-Garawi,A., Mak,S., Lora,J.M., Briskin,M., Jurman,M., Cao,J.,
DiStefano,P.S. and Bertin,J.

TITLE PYPAF1, a PYRIN-containing Apaf1-like protein that assembles with
ASC and regulates activation of NF-kappa B

JOURNAL J. Biol. Chem. 277 (13), 11570-11575 (2002)

PUBMED [11786556](#)

REFERENCE 17 (bases 1 to 4484)

AUTHORS Hoffman,H.M., Mueller,J.L., Broide,D.H., Wanderer,A.A. and
Kolodner,R.D.

TITLE Mutation of a new gene encoding a putative pyrin-like protein
causes familial cold autoinflammatory syndrome and Muckle-Wells
syndrome

JOURNAL Nat. Genet. 29 (3), 301-305 (2001)

PUBMED [11687797](#)

REFERENCE 18 (bases 1 to 4484)

AUTHORS Hoffman,H.M., Wright,F.A., Broide,D.H., Wanderer,A.A. and
Kolodner,R.D.

TITLE Identification of a locus on chromosome 1q44 for familial cold
urticaria

JOURNAL Am. J. Hum. Genet. 66 (5), 1693-1698 (2000)

PUBMED [10741953](#)

COMMENT REVIEWED [REFSEQ](#): This record has been curated by NCBI staff. The
reference sequence was derived from [AF410477.1](#) and [AF054176.1](#).
On Sep 22, 2003 this sequence version replaced [gi:19923283](#).

Summary: This gene encodes a pyrin-like protein which contains a
pyrin domain, a nucleotide-binding site (NBS) domain, and a
leucine-rich repeat (LRR) motif. This protein interacts with
apoptosis-associated speck-like protein containing a CARD. Proteins
which contain the caspase recruitment domain, CARD, have been shown
to be involved in inflammation and immune response. This protein
may function as an activator of NF-kappaB signaling. The encoded
protein may play a role in the regulation of inflammation and
apoptosis. Mutations in this gene have been associated with
familial cold autoinflammatory syndrome (FCAS), Muckle-Wells
syndrome (MWS), chronic infantile neurological cutaneous and
articular (CINCA) syndrome, and neonatal-onset multisystem
inflammatory disease (NOMID). Two transcript variants encoding
distinct isoforms have been identified for this gene.

Transcript Variant: This variant (1) represents the longer
transcript and encodes the longer isoform (a).

FEATURES

source Location/Qualifiers

1..4484

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:[9606](#)"

/chromosome="1"

/map="1q44"

gene

1..4484

/gene="CIAS1"

/note="synonyms: FCU, MWS, FCAS, NALP3, Clorf7, PYPAF1,
AII/AVP, AGTAVPRL"

/db_xref="GeneID:[114548](#)"

/db_xref="HGNC:[16400](#)"

/db_xref="HPRD:[05915](#)"

/db_xref="MIM:[606416](#)"

CDS

747..3857

/gene="CIAS1"

```
/note="isoform a is encoded by transcript variant 1;  
chromosome 1 open reading frame 7; angiotensin/vasopressin  
receptor AII/AVP-like; NACHT, LRR and PYD containing  
protein 3; cryopyrin; AII/AVP receptor-like;  
PYRIN-containing APAF1-like protein 1; Muckle-Wells  
syndrome;  
go_component: cellular component\unknown [goid 0008372]  
[evidence NAS] [pmid 12093792];  
go_process: apoptosis [goid 0006915] [evidence IEA];  
go_process: signal transduction [goid 0007165] [evidence  
NAS] [pmid 11786556];  
go_process: inflammatory response [goid 0006954] [evidence  
IMP] [pmid 12093792];  
go_process: induction of apoptosis [goid 0006917]  
[evidence NAS] [pmid 12032915];  
go_process: sensory perception of sound [goid 0007605]  
[evidence IEA]"  
/codon_start=1  
/product="cryopyrin isoform a"  
/protein_id="NP_004886.3"  
/db_xref="GI:34878693"  
/db_xref="CCDS:CCDS1632.1"  
/db_xref="GeneID:114548"  
/db_xref="HGNC:16400"  
/db_xref="HPRD:05915"  
/db_xref="MIM:606416"  
/translation="MKMASTRCKLARYLEDLEDVDLKKFKMHLEDYPPQKGCIPLPRG  
QTEKADHVDLATLMIDFNGEKAWAMAVWIFAAINRRDLYEKAKRDEPKWGS DNARVS  
NPTVICQEDSIEEEWMGLLEYLSRISICKMKKDYRKRYRKYVRSRFQCIEDRNARLGE  
SVSLNKRYTRLRLIKEHRSQQEREQELLAIGKTKTCESPVSPKIMELLFDPDDEHSEP  
VHTVVFQGAAGIGKTI LARKMMLDWASGTL YQDRFDYLFYIHCREVSLVTQ RSLGDLI  
MSCCPDPNPP IHKIVRKPSRILFLMDGFDELQGA FDEHIGPLCTDWQKAERGDILLSS  
LIRK KLLPEASLLITR PVALEKLQHLLDHPHVEILGFSEAKRKEYFFKYFSDEAQA  
RAAFSLIQENEVLFTMCFIPLVCWIVCTGLKQQMESGKSLAQTSKTTTAVYVFFLSSL  
LQPRGGSQEHLCAHLWGLCSLAADGIWNQKILFEESDLRNHGLQKADVSAFLRMNLF  
QKEVDCEKFYSFIHMTFQEFFAAMYLLLEEKEGRTNVP GSRLKLP SRDVTVLLENYG  
KFEKGYLIFVVRFLFGLVNQERTSYLEKKLSCKISQQIRLELLKWIEVKAKAKKLQIQ  
PSQLELFYCLYEMQEEDFVQRAMDYFPKIEINLSTRMDH MVSSF CIENCHRVESLSLG  
FLHNMPKEEEEEKEGRHLD MVQC VLPSSSHAACSHGLVNSHLTSSFCRGLFSVLSTS  
QSLTELDLSDNSLGD PGM RVL CETLQH PGCNIRRLWLGR CGLSHECCFDISLVLSSNQ  
KLVELDLSDNALGDFGIRLLCVGLKHLLCNLKKLWLVSCCLTSACCQDLASVLSTSHS  
LTRLYVGENALGDSGVAILCEKAKNPQC NLQKLGLVNSGLTSVCCSALSSVLSTNQNL  
THLYLRGNTLGDKGIKLLCEGLLHPDCKLQVLELDNCNLTS HCCWDLSTLLTSSQSLR  
KLSLGNNDLGD LGVMMFCEVLKQQSCLLQNLGLSEMYFNYETKSALETLQEEKPELTV  
VFEP SW"  
misc feature 780..995  
/gene="CIAS1"  
/note="Region: pyrin domain"  
misc feature 1395..2345  
/gene="CIAS1"  
/note="Region: NBS (NACHT) domain"  
misc feature 2835..3848  
/gene="CIAS1"  
/note="Region: leucine-rich repeat domain"  
STS 4098..4243  
/gene="CIAS1"  
/standard_name="SHGC-76649"  
/db_xref="UniSTS:70843"  
polyA signal 4149..4154  
/gene="CIAS1"
```

polyA site 4170
 /gene="CIAS1"
polyA signal 4429..4434
 /gene="CIAS1"
polyA site 4461
 /gene="CIAS1"

ORIGIN

```

1 gtagatgagg aaactgaagt tgaggaatag tgaagagttt gtccaatgtc atagccccgt
61 aatcaacggg acaaaaattt tcttgctgat gggcaagat ggcacgtga agtgggtgtt
121 caccgtaaac tgtaatacaa tcttgtttat ggatttgttt gcatattttt ccctccatag
181 ggaaaccttt cttccatggc tcaggacaca ctcttggtat gagccaacag gagaactttc
241 tggtaagcat ttggctaact tttttttttt tgagatggag tcttgctgtg tcgcctaggc
301 tggagtgcag tggcgtgatc ttggctcact gcagcctcca cttcccgggt tcaatcaatt
361 ctctacctc aacttcctga gtagctggga ttacaggcgc ccgccaccac acccggtcca
421 tttttgtact tttagtagag acacagtttt gccatgttgg ccaggctggt cttgaattcc
481 tcagctcagg tgatctgcct gccttggcct ctcaaagtgc tgggattaca ggcgtgagcc
541 actgtgcccg gccttggcta acttttcaaa attaaagatt ttgacttggt acagtcatgt
601 gacatttttt tctttctgtt tgctgagttt tgataattt atatctctca aagtggagac
661 tttaaaaaag actcatccgt gtgccgtgtt cactgcctgg tatcttagtg tggaccgaag
721 cctaaggacc ctgaaaacag ctgcagatga agatggcaag caccgctgc aagctggcca
781 ggtacctgga ggacctggag gatgtggact tgaagaaatt taagatgcac ttagaggact
841 atcctcccca gaagggtgc atccccctcc cgaggggtca gacagagaag gcagaccatg
901 tggatctagc cacgctaata atcgacttca atggggagga gaaggcgtgg gccatggccg
961 tgtggatctt cgctgcgatc aacaggagag acctttatga gaaagcaaaa agagatgagc
1021 cgaagtgggg ttcagataat gcacgtgttt cgaatccac tgtgatatgc caggaagaca
1081 gcattgaaga ggagtggatg ggtttactgg agtacctttc gagaatctct atttgtaaaa
1141 tgaagaaaga ttaccgtaag aagtacagaa agtacgtgag aagcagattc cagtgcattg
1201 aagacaggaa tgcccgtctg ggtgagagtg tgagcctcaa caaacgctac acacgactgc
1261 gtctcatcaa ggagcaccgg agccagcagg agagggagca ggagcttctg gccatcgcca
1321 agaccaagac gtgtgagagc cccgtgagtc cattaagat ggagtgtctg tttgaccccg
1381 atgatgagca ttctgagcct gtgcacaccg tgggtgttcca gggggcggca gggattggga
1441 aaacaatcct ggccaggaag atgatgttgg actgggcgtc ggggacactc taccaagaca
1501 ggtttgacta tctgttctat atccactgtc gagaggtag ccttgtgaca cagaggagcc
1561 tgggggacct gatcatgagc tgctgccccg acccaaacc acccatccac aagatcgtga
1621 gaaaaccctc cagaatcctc ttcctcatgg acggcttcga tgagctgcaa ggtgcctttg
1681 acgagcacat aggaccgtc tgactgact ggcagaaggc cgagcgggga gacattctcc
1741 tgagcagcct catcagaaag aagctgtctc ccgaggcctc tctgtctatc accacgagac
1801 ctgtggccct ggagaaactg cagcacttgc tggaccatcc tcggcatgtg gagatcctgg
1861 gtttctccga ggccaaaagg aaagagtact tcttcaagta cttctctgat gaggcccaag
1921 ccagggcagc cttcagctg attcaggaga acaggtcct cttcaccatg tgcttcatcc
1981 ccctggtctg ctggatcgtg tgactggagc tgaaacagca gatggagagt ggcaagagcc
2041 ttgccagac atccaagacc accaccgagg tgtacgtctt cttcctttcc agtttgctgc
2101 agccccgggg agggagccag gagcacggcc tctgcgcca cctctggggg ctctgctctt
2161 tggctgcaga tggaatctgg aaccagaaaa tctgttttga ggagtccgac ctcaggaatc
2221 atggactgca gaaggcggat gtgtctgctt tcctgaggat gaacctgttc caaaaggaag
2281 tggactgcga gaagtcttac agcttcatcc acatgacttt ccaggagttc tttgccgcca
2341 tgtactacct gctggaagag gaaaaggaag gaaggacgaa cgttccaggg agtcgtttga
2401 agcttcccag ccgagacgtg acagtctctc tggaaaacta tggcaaattc gaaaaggggt
2461 atttgatatt tgttgtagct tctctctttg gcctggtaaa ccaggagagg acctcctact
2521 tggagaagaa attaagttgc aagatctctc agcaaatcag gctggagctg ctgaaatgga
2581 ttgaagtga agccaaagct aaaaagctgc agatccagcc cagccagctg gaattgttct
2641 actgtttgta cgagatgcag gaggaggact tcgtgcaaag ggcatggac tatttcccca
2701 agattgagat caatctctcc accagaatgg accacatggt ttcttccttt tgcattgaga
2761 actgtcatcg ggtggagtca ctgtccctgg ggtttctcca taacatgccc aaggaggaag
2821 aggaggagga aaaggaaggc cgacaccttg atatggtgca gtgtgtcctc ccaagctcct
2881 ctcatgctgc ctgttctcat ggattggtga acagccacct cacttccagt ttttgccggg
2941 gcctcttttc agttctgagc accagccaga gtctaactga attggacctc agtgacaatt
3001 ctctggggga cccagggatg agagtgttgt gtgaaacgct ccagcatcct ggctgtaaca
3061 ttcggagatt gtggttgggg cgctgtggcc tctcgcatga gtgctgtctc gacatctcct
3121 tggctctcag cagcaaccag aagctggtgg agctggacct gagtgaacac gccctcgggtg
  
```

```
3181 acttcggaat cagacttctg tgtgtgggac tgaagcacct gttgtgcaat ctgaagaagc
3241 tctgggttggc cagctgctgc ctcacatcag catgttgtca ggatcttgca tcagtattga
3301 gcaccagcca ttccctgacc agactctatg tgggggagaa tgccttggga gactcaggag
3361 tcgcaatttt atgtgaaaaa gccagaatc cacagtgtaa cctgcagaaa ctgggggttg
3421 tgaattctgg ccttacgtca gtctgttggt cagctttgtc ctgggtactc agcactaatc
3481 agaatctcac gcacctttac ctgcgaggca aactctcgg agacaagggg atcaaactac
3541 tctgtgaggg actcttgcac ccgactgca agcttcagg gttggaatta gacaactgca
3601 acctcacgtc aactgctgc tgggatcttt ccacacttct gacctccagc cagagcctgc
3661 gaaagctgag cctgggcaac aatgacctgg ggcacctggg ggtcatgatg ttctgtgaag
3721 tgctgaaaca gcagagctgc ctctgcaga acctgggggt gtctgaaatg tatttcaatt
3781 atgagacaaa aagtgcgtta gaaacacttc aagaagaaaa gcctgagctg accgtcgtct
3841 ttgagccttc ttggtaggag tggaaacggg gctgccagac gccagtgttc tccgggtccct
3901 ccagctgggg gccctcagg gtagagagct gcgatccatc caggccaaga ccacagctct
3961 gtgatccttc cgggtggagt tcggagaaga gagcttgccg acgatgcctt cctgtgcaga
4021 gcttgggcat ctcttttacg ccagggtgag gaagacacca ggacaatgac agcatcgggt
4081 gttgttgtca tcacagcgcc tcagttagag gatgttcctc ttggtgacct catgtaatta
4141 gtcattcaa taaagcactt tctttatctt tctcttctct gtctaacttt ctttttccta
4201 tcttttttct tctttgttct gtttactttt gctcatatca tcattcccgc tatctttcta
4261 ttaactgacc ataacacaga actagttgac tatatattat gttgaaattt tatggcagct
4321 atttatttat ttaaattttt tgtaacagtt ttgttttcta ataagaaaaa tccatgcttt
4381 ttgtagctgg ttgaaaattc aggaatatgt aaaacttttt ggtatttaat taaattgatt
4441 ccttttctta attttaaaaa aaaaaaaaaa aaaaaaaaaa aaaa
```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42



My NCBI
[Sign In](#)
[Register](#)

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Limits Preview/Index History Clipboard Details

Display ☒ Show ☒ Send to ☒Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒☐ 1: [NM_024618](#). Reports Homo sapiens NOD9...[gi:25777607][Links](#)

LOCUS NM_024618 3761 bp mRNA linear PRI 10-JUN-2005
DEFINITION Homo sapiens NOD9 protein (NOD9), transcript variant 1, mRNA.
ACCESSION NM_024618
VERSION NM_024618.2 GI:25777607
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM [Homo sapiens](#)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 3761)
AUTHORS Inohara,N. and Nunez,G.
TITLE NODs: intracellular proteins involved in inflammation and apoptosis
JOURNAL Nat. Rev. Immunol. 3 (5), 371-382 (2003)
PUBMED [12766759](#)
REMARK Review article
COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The
reference sequence was derived from [BC023974.2](#).
On Nov 27, 2002 this sequence version replaced [gi:13375837](#).

Summary: Alternative splicing has been observed at this gene locus and two transcript variants, encoding distinct isoforms, have been identified. The function of this protein has not been determined.

Transcript Variant: This variant (1) represents the longer transcript and encodes the longer isoform (1).

COMPLETENESS: complete on the 3' end.

FEATURES

	Location/Qualifiers
source	1..3761 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /chromosome="11" /map="11q23.3"
gene	1..3761 /gene="NOD9" /note="synonyms: FLJ21478, MGC21025" /db_xref="GeneID:79671"
CDS	240..3167 /gene="NOD9" /note="isoform 1 is encoded by transcript variant 1" /codon_start=1 /product="NOD9 protein isoform 1" /protein_id="NP_078894.2" /db_xref="GI:25777608"

/db_xref="CCDS:CCDS8416.1"
/db_xref="GeneID:79671"
/translation="MRWGHHLPRASWGSFRRALQRPDDRIPFLIHWSWPLQGERPFG
PPRAFIRHHGSSVDSAPPPGRHGRLFPSASATEAIQRHRRNLAWF SRLPREERQFGP
TFALD TVHVPVIRESTPDELLRPPAELALEHQPPQAGLPPLALSQLFNPDACGRRVQ
TVVLYGTVGTGKSTLVRKMLVDWCYGRLPAPFELLIPFSCEDLSSLGPPASLCLVAQ
RYTPLKEVLP LMAAAGSHLLFVLHGLEHLNLD FRLAGTGLCSDPEEPQEPAAIIVNLL
RKYMLPQASILVTTRPSAIGRIPSKYVGRYGEICGFSDTNLQKLYFQLRLNQPYCGYA
VGGSGVSATPAQRDHLVQMLSRNLEGHQIAAACFLPSYCWLV CATLHFLHAPT PAGQ
TLTSIYTSFLRLNFSGETLDSTDPSNLSLMAYAARTMGKLAYEGVSSRKTYFSEEDVC
GCLEAGIRTEEEFQLLHIFRDLALRFFLAPC VEPGRAGTFVFTVPAMQEYLAALYIVL
GLRKTTLQKVGKEVAELVGRVGEDVSLVLGIMAKLLPLRALPLLNLIKVVP RVFGRM
VGKSREAVAQAMVLEMFREEDY YNDDVLDQMGASILGVEGPRRHPDEPPEDEVFELFP
MFMGGLLSAHNRAVL AQLGCP IKNLDALENAQAIKKKLGKLGROVLPPSELLDHLFFH
YEFQNRFSAEVLS SLRQLNLAGVRMTPVKCTVVA AVLGSGRHALDEVN LASCQLDPA
GLRTL LPVFLRARKLGLQLNSLGPEACKDLRD LLLHDQCQITTLRLSNNPLTAAGVAV
LMEGLAGNTSVTHLSLLHTGLGDEGLELLAAQLDRNRQLQELNVAYNGAGDTAALALA
RAAREHPSLELLHLYFNELSS EGRQVLRDLGGAAEGGARVVVSLTEGTAVSEYWSVIL
SEVQRNLNSWDRARVQRHLELLLRDLEDSRGATLNPWRKAQLLRVEGEVRALLEQLGS
SGS"
STS 3579..3728
/gene="NOD9"
/standard_name="WI-16056"
/db_xref="UniSTS:53534"
polyA signal 3718..3723
/gene="NOD9"
polyA site 3744
/gene="NOD9"
/experiment="experimental evidence, no additional details
recorded"

ORIGIN




```
1  cgcggggatg  gaggcaggga  ggggggacga  tggcgggacg  ggtggcgccg  gggttccage
61  cctgcgcctg  ctccggagca  ccggggccct  ctcgctgacc  ccctcgtccc  aggaccccgc
121 aggcccagat  gcctgggctc  gtcctctttc  gcgcccgtg  ccaggtgcca  gggccgcgca
181 ggcgggcgga  ggacagaagt  cggtcctagg  cccccaggc  tctgaccttc  tttcccagga
241 tgagggtggg  ccaccatttg  cccaggccct  cttggggctc  tggttttaga  agagcactcc
301 agcgaccaga  tgatcgatc  cccttctga  tccactggag  ttggccctt  caaggggagc
361 gtcccttttg  gccccctagg  gcctttatac  gccaccagg  aagctcgga  gatagcgtc
421 cccacccgg  gaggcattga  cggtgttcc  ccagcgctc  tgcaactgaa  gctatacagc
481 ggcaccgccc  gaacctggct  gagtggttca  gccggctgcc  caggaggagg  cgccagtttg
541 gcccacctt  tgccctagac  acggtccacg  ttgacctgt  gatccgcgag  agtaccctg
601 atgagctact  tcgcccaccc  gcggagctgg  ccctggagca  tcagccaccc  caggccgggc
661 tccccccact  ggccttgtct  cagctcttta  acccggtatg  ctgtgggctc  cgggtgcaga
721 cagtgggtgt  gtatgggaca  gtgggcacag  gcaagagcac  gctgggtgct  aagatgggtc
781 tggactggtg  ttatgggcgg  ctgcccgcct  tcgagctgct  catcccttc  tcctgtgagg
841 acctgtcatc  cctgggccct  gcccagcct  ccctgtgcca  acttgtggcc  cagcgtaca
901 cgcccctgaa  ggaggttctg  cccctgatgg  ctgctgctgg  gtcccacctc  ctctttgtgc
961 tccatggctt  agagcatctc  aacctcgact  tccggctggc  aggcacggga  ctttgtagt
1021 acccgaggga  accgcaggaa  ccagctgcta  tcatcgtcaa  cctgctgctc  aaatacatgc
1081 tgccctagge  cagcattctg  gtgaccactc  ggccctctgc  cattggccgt  atccccagca
1141 agtacgtggg  ccgctatggt  gagatctgct  gtttctctga  taccaacctg  cagaagctct
1201 acttccagct  ccgctcaac  cagccgtact  gcgggtatgc  cgttggcggg  tcaggtgtct
1261 ctgccacacc  agctcagcgt  gaccacctgg  tgcagatgct  ctcccgaac  ctggaggggc
1321 accaccagat  agccgctgcc  tgcttctctg  cgtcctattg  ctggctcgtt  tgtgccacct
1381 tgcacttctt  gcatgcccc  acgcctgctg  ggcagaccct  tacaagcatc  tataccagct
1441 tcctgctgct  caacttcagc  ggggaaaccc  tggacagcac  tgaccctcc  aatttgtccc
1501 tgcagcccta  tgcagcccta  accatgggca  agttggccta  tgaggggggt  tcctcccga
1561 agacctactt  ctctgaagag  gatgtctgtg  gctgcctgga  ggctggcatc  aggacggagg
1621 aggagtttca  gctgctgcac  atcttccgtc  gggatgccct  gaggttttcc  ctggcccat
1681 gtgtggagcc  agggcggtga  ggcaccttcg  tgttcaccgt  gcccgccatg  caggaatacc
```

1741 tggctgccct ctacattgtg ctgggtttgc gcaagacgac cctgcaaaag gtgggcaagg
1801 aagtggctga gctcgtgggc cgtgttgggg aggacgtcag cctgggtactg ggcacatcatgg
1861 ccaagctgct gcctctgcgg gctctgcctc tgctcttcaa cctgatcaag gtggttccac
1921 gagtggttgg gcgcatggtg ggtaaaagcc gggaggcggg ggctcaggcc atggtgctgg
1981 agatgtttcg agaggaggac tactacaacg atgatgttct ggaccagatg ggcgccagta
2041 tcctgggctg ggagggcccc cggcgccacc cagatgagcc ccctgaggat gaagtcttcg
2101 agctcttccc catgttcatg ggggggcttc tctctgcca caaccgagct gtgctagctc
2161 agcttggctg ccccatcaag aacctggatg ccctggagaa tgcccaggcc atcaagaaga
2221 agctgggcaa gctgggcccgg caggtgctgc ccccatcaga gctccttgac cacctcttct
2281 tccactatga gttccagaac cagcgcttct ccgctgaggt gctcagctcc ctgctcagc
2341 tcaacctggc aggtgtgcgc atgacaccag tcaagtgcac agtgggtggc gctgtgctgg
2401 gcagcgggaag gcatgccctg gatgaggtga acttggcctc ctgccagcta gatcctgctg
2461 ggctgcgcac actcctgcct gtcttctctg gtgcccggaa gctgggcttg caactcaaca
2521 gcctgggccc tgaggcctgc aaggacctcc gagacctgtt gctgcatgac cagtgccaaa
2581 ttaccacact gcggctgtcc aacaaccgc tgacggcggc aggtgttgcc gtgctaattg
2641 aggggctggc aggaacacc tcagtgcgc acctgtccct gctgcacacg ggccttgggg
2701 acgaaggcct ggagctgctg gctgcccagc tggaccgcaa ccggcagctg caggagctga
2761 acgtggcgta caacggtgct ggtgacacag cggccctggc cctggccaga gctgcccggg
2821 agcacccttc cctggaactg ctacacctct acctcaatga gctgagctca gaggccgccc
2881 aggtcttgcg agacttgggg ggtgctgctg aagggtgtgc ccgggtggtg gtgtcactga
2941 cagaggggac ggcggtgtca gaatactggt cagtgatcct cagtgaagtc cagcgggaacc
3001 tcaatagctg ggatcgggcc cgggttcagc gacaccttga gctcctactg cgggatctgg
3061 aagatagccg gggtgccacc cttaatcctt ggcgcaaggc ccagctgctg cgagtggagg
3121 gcgaggtcag ggcctcctg gagcagctgg gaagctctgg aagctgagac actggcggca
3181 ggcacctagc tatgtgacca ctggccctaa accttttccc tctgtggcct cctggcttgc
3241 actgctccct ctagaaagat tccttcaggt ctggaggcag aggaatgggc atagctgagc
3301 cagttgccct cctagggcat gtttgaccag gactgagtct ggaatctcca agttaagat
3361 ggtgaatcaa tgcttcgggc ttggagatgg aacatgcctc ctctccattc agctagaagg
3421 accaaagcat gtggcatttg gatggccaga gtgccctgaa gcaccactac caaccttgcc
3481 tccccctcct ctcaaagagc ctctgactgt gtcaccaagg ggctcacatc ttatgtctgc
3541 catgccaggg gtgtcgccat ccagatgtgt tgggaagcttc ccctcctgcc ttatgtctac
3601 ctgtggacac cgaggatgcc ctcacattgg tgctttctcc tcacctcat gcccccttg
3661 ccacaatggt atgatggctt ggtagccctc cgaggcagat gcacctgact tgctgctatt
3721 aaaaagccgt gtgccttcta ccaaaaaaaaa aaaaaaaaaa a

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search  for  

Limits Preview/Index History Clipboard Details

Display **GenBank** Show **5** Send to

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [NM_145827](#). Reports *Mus musculus* cold...[gi:48675839] [Links](#)

LOCUS NM_145827 4022 bp mRNA linear ROD 18-OCT-2005

DEFINITION Mus musculus cold autoinflammatory syndrome 1 homolog (human) (Cias1), mRNA.

ACCESSION NM 145827

VERSION NM 145827.2 GI:48675839

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 4022)

AUTHORS Anderson, J.P., Mueller, J.L., Rosengren, S., Boyle, D.L., Schaner, P., Cannon, S.B., Goodyear, C.S. and Hoffman, H.M.

TITLE Structural, expression, and evolutionary analysis of mouse CIAS1

JOURNAL Gene 338 (1), 25-34 (2004)

PUBMED 15302403

REMARK GeneRIF: C1A1 mRNA expression found primarily in peripheral blood leukocytes consistent with the postulated inflammatory function.

REFERENCE 2 (bases 1 to 4022)

AUTHORS Kikuchi-Yanoshita, R., Taketomi, Y., Koga, K., Sugiki, T., Atsumi, Y., Saito, T., Ishii, S., Hisada, M., Suzuki-Nishimura, T., Uchida, M.K., Moon, T.C., Chang, H.W., Sawada, M., Inagaki, N., Nagai, H., Murakami, M. and Kudo, I.

TITLE Induction of PYPAF1 during in vitro maturation of mouse mast cells

JOURNAL J. Biochem. 134 (5), 699-709 (2003)

PUBMED 14688236

REMARK GeneRIF: MMIG-1, a likely mouse PYPAF1 ortholog, may play a role in mast cell-directed inflammatory diseases

REFERENCE 3 (bases 1 to 4022)

AUTHORS Albrecht, M., Domingues, F.S., Schreiber, S. and Lengauer, T.

TITLE Identification of mammalian orthologs associates PYPAF5 with distinct functional roles

JOURNAL FEBS Lett. 538 (1-3), 173-177 (2003)

PUBMED 12633874

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
NCBI review. The reference sequence was derived from AY495376.1.
On Jun 13, 2004 this sequence version replaced gi:22003869.

```
FEATURES                                Location/Qualifiers
     source                               1..4022
                                     /organism="Mus musculus"
                                     /mol_type="mRNA"
                                     /strain="BALB/c"
                                     /db_xref="taxon:10090"
                                     /chromosome="11"
```


gene 1..4022
 /gene="Cias1"
 /note="synonyms: FCU, MWS, FCAS, Mmig1, NALP3, Pypaf1, AII/AVP, AGTAVPRL"
 /db_xref="GeneID:216799"
 /db_xref="MGI:2653833"
CDS 227..3328
 /gene="Cias1"
 /note="cryopyrin; mast cell maturation inducible protein 1; NACHT/LRR/pyrin domain-containing protein 3;
 go_process: apoptosis [goid 0006915] [evidence IEA]"
 /codon_start=1
 /product="cold autoinflammatory syndrome 1 homolog"
 /protein_id="NP_665826.1"
 /db_xref="GI:22003870"
 /db_xref="GeneID:216799"
 /db_xref="MGI:2653833"
 /translation="MTSVRCKLAQYLEDLEDVDLKKFKMHLEDYPPEKGCIPVPRGQM
 EKADHLDLATLMIDFNGEKAWAMAVWIFAAINRRDLWEKAKKDQPEWNTCTSHSSM
 VCQEDSLEEEWMGLLGYSRISICKKKKDYCKMYRRHVRSRFYSIKDRNARLGESVDL
 NSRYTQLQLVKEHPSKQEREHELLTIGRTKMRDSPMSSLKLELLFEPEDGHSEPVHTV
 VFQGAAGIGKTILARKIMLDWALGKLFKDKFDYLFHICREVSRLTPRSLADLIVSCW
 PDPNPPVCKILRKPSRILFLMDGFDELQGAFFDEHIGEVCTDWQKAVRGDILLSSLIRK
 KLLPKASLLITTRPVALEKLQHLLDHPHVEILGFSEAKRKEYFFKYFSNELQAREAF
 RLIQENEVLFTMCFIPLVCWIVCTGLKQOMETGKSLAQTSKTTTAVYVFFLSSLLQSR
 GGIEEHLFSDYLQGLCSLAADGIWNQKILFEEDLRKHGLQKTDVSAFLRMNVFQKEV
 DCERFYSFSHMTFQEFFAAMYILLEEEAEGETVRKGPGGCSDLLNRDVKVLLLENYKGF
 EKGYLIFVVRFLFGLVNQERTSYLEKKLSCKISQQVRLELLKWIEVKAKAKKLQWQPS
 QLELFYCLYEMQEEDFVQSAMDHFPKIEINLSTRMDHVSVSFCIKNCHRVKTLNLSLGGF
 HNSPKEEEEERRGGRPLDQVQCVFPDTHVACSSRLVNCCLTSSFCRGLFSSLSLSTNRSL
 TELDLSDNLTGDPGMRVLCEALQHPGCNIQRLWLGRCLSHQCCFDISSVLSSSQKL
 ELDLSDNALGDFGIRLLCVGLKHLNQLKWLVSCLTSACQDLALVLSSNHSLTR
 LYIGENALGDSGVQVLCEKMKDPQCNLQKLGLVNSGLTSICCSALTSVLKTNQNFTHL
 YLRNALGDTGLRLLCEGLLHPDCKLQMLELDNCSLTSHSCWNLSLTILTHNHSRKLN
 LGNNDLGDLCVVTLCVVLKQQGCLLQSLQLGEMYNLRETKRALEALQEEKPELTIVFE
 ISW"
polyA signal 3997..4002
 /gene="Cias1"

ORIGIN

```

1  ccaggtccta ccctcgtcac catgggttct ggtcagacac gagtccctggt gactttgtat
61 atgcgtgttc tctgtatacc acatctgatt gtgttaatgg ctttcttatt tttatctcta
121 cagaggaact tttcttccat ggctcaggac atacgtctgg atcaagctaa gagaactttc
181 tgtgtggacc taagccccga gacctcgaa agggctgctg ctgaagatga cgagtgtccg
241 ttgcaagctg gctcagtatc tagaggacct tgaagatgtg gacctcaaga aattcaaaat
301 gcatttggaa gattaccgcg ccgagaaaagg ctgtatccca gtccccaggg gccagatgga
361 gaaggcagat cacttggatc tagccacact catgattgac ttcaatggcg aggagaaggc
421 ctgggccatg gctgtgtgga tctttgctgc gatcaacagg cgagacctct gggaaaaagc
481 taagaaggac cagccagagt ggaatgacac gtgtacatca cattcctcta tggtagcca
541 ggaggacagc cttgaagaag agtggatggg tttgctggga tatctctccc gcatctccat
601 ttgtaaaaag aagaaagatt actgtaagat gtacagacga catgtgagaa gcaggttcta
661 ctctatcaag gacaggaacg cgcgtctagg tgagagtgtg gacctcaaca gtcgctacac
721 gcagctccaa ctggtcaagg agcatccaa caagcaggag cgggagcatg aactcctgac
781 catcggccgg actaaaatgc gggacagccc catgagttcc cttaaagctg agctgctgtt
841 tgagcccag gacgggcact cggagcctgt gcacacagt gtgttcagg gggcagcagg
901 catcgggaaa accatcctag ccaggaagat tatgttggac tgggcactgg gaaagctctt
961 caaagacaaa tttgactatt tgttctttat ccactgccga gaggtgagcc tcaggacgcc
1021 aaggagtcta gcagacctga ttgtcagctg ctggcctgac ccaaaccac cagtgtgcaa
1081 gatcctgcgc aagccttcca ggatcctctt cctcatggat ggctttgatg agctacaagg
1141 ggcctttgac gagcacattg gggaggtctg cacagactgg caaaaggctg tgcggggaga
1201 cattctgcta agcagcctca tccgaaaagaa actgctgccc aaggcctctc tgctcataac


```

```
1261 gacgaggccg gtagccttgg agaaactgca gcatctcctg gaccaccccc gccatgtgga
1321 gatcctaggt ttctctgagg ccaaaaggaa ggagtatttc ttttaagtatt tctccaacga
1381 gctgcaggcc cgggaggcct tcaggctgat ccaagagaat gaggtcctct ttaccatgtg
1441 cttcatcccc ctggtctgct ggattgtgtg cacggggcta aagcaacaga tggagaccgg
1501 gaagagcctg gcccagacct ccaagaccac tacggccgctc tacgtcttct tcttttccag
1561 cctgctgcaa tcccgggggg gcattgagga gcatctcttc tctgactacc tacaggggct
1621 ctgttcaactg gctgcggatg gaatttgga ccagaaaatc ctatttgagg agtgtgatct
1681 gcggaagcac ggccctgcaga agactgacgt ctccgctttc ctgaggatga acgtgttcca
1741 gaaggaagtg gactgcgaga gattctacag cttcagccac atgactttcc aggagttctt
1801 cgctgctatg tactatttgc tggaagagga ggcagagggg gagaccgtga ggaaaggacc
1861 aggaggttgt tcagatcttc tgaaccgaga cgtgaaggctc ctactagaaa attacggcaa
1921 gtttgaaaaa ggctatctga tttttgttgt ccgattcctc tttggccttg taaaccagga
1981 gagaacctct tatttggaaga agaaactaag ttgcaagatc tctcagcaag tcagactgga
2041 actactgaag tggattgaag tgaaagccaa ggccaagaag ctgcagtggc agcccagcca
2101 actggaactg ttctactgcc tgtacgagat gcaggaggaa gactttgtgc agagtgccat
2161 ggaccacttt cccaaaattg agatcaacct ctctaccaga atggaccacg tggtttcttc
2221 cttttgtatt aagaactgtc atagggtcaa aacgctttcc ctgggttttt ttcacaactc
2281 gccaaggag gaagaagaag agaggagagg aggtcgacct ttggaccagg ttcagtgtgt
2341 tttcccagac actcatgttg cctgttcttc cagactgggtg aactgctgcc tcacttctag
2401 cttctgccgt ggtctcttct caagtctaag caccaaccgg agcctcactg aactggacct
2461 cagtgaacaat actctgggag acccgggcat gaggggtgctg tgtgaggcac tccagcacc
2521 aggtctgaac attcagagac tgtggttggg gcgctgcgga ctgtcccatc aatgctgctt
2581 cgacatctcc tctgtcctga gcagcagcca gaagctgggtg gagctggacc tcagtgacaa
2641 tgccctgggg gactttggaa tcagattgct gtgtgtggga ctgaagcacc tgctctgcaa
2701 cctccagaaa ctgtggttgg tgagctgctg tctcacatcc gcgtgtgtgc aggatctcgc
2761 attggttctg agctccaacc attctctgac cagactgtac attggagaaa atgccttggg
2821 agactcagga gtccaagttt tgtgtgaaaa gatgaaggac ccacagtgtg acttgcagaa
2881 gctgggggtg gtgaattccg gccttacttc aatctgttgt tcagctctga cctctgtgct
2941 caaaaccaac cagaacttca cacacctcta tctacgaagc aatgcccttg gagacacagg
3001 actcaggctc ctctgtgagg ggcttctgca cccggactgt aaactacaga tgctggaatt
3061 agacaactgc agcctcacct cacacagctg ctggaatctc tccacaattc tgaccacaa
3121 ccacagcctt cggaaagctga acctgggcaa caatgatctt ggcgatctgt gcgtggtgac
3181 cctctgtgag gtgctgaaac agcagggctg cctcctgcag agcctacagt tgggtgaaat
3241 gtacttaaat cgtgaaacaa aacgtgcctt agaagcgctc caggaagaaa agcctgagct
3301 gactatagtc ttcgagattt cctggtaggc gtggaagcag gaccaccagg tgccctcggtc
3361 ctgccccaa gtcctgcccc agccccagtg cgcactgctc ttcactgcta tcaagccctc
3421 cttcaccatc aggatcacag ccgaggctct tctggtatag ggtctggagc aaaggcttgt
3481 gtgggaccaa atatttttcc tcacatcgat aacgtgaaac tgccagaggc tgcccttccc
3541 atcatatcct cagtgggcaa ggtgttccct cttggtgact tcatggaaac agcttcaaga
3601 aaacgccttt tcttgtcctc ccccgccctc ctcttactcc tgccctcctc cctcctcctc
3661 ctccccctcc cccccctcct cctccgcttc tccccccacc tgtctttctc tctctgggac
3721 tctggttttt tgacctttgc ccataccttc agtcttgtct tctgtttaac tgaccatccc
3781 gcataaggag ctgcccgtgg gctagatgga aggtttgtgg cagcctctca gctacattgt
3841 ttgtttttat tttttaatag ttatgatttc tcttttagcta cctgaaaact cagagattta
3901 taaaacccat ttttgtattt attgtatgtt tgtactgctt tcttaattta aaaatgtatc
3961 tagaattctt ttaagttatt tatccaaact actaaaaata aatcagttta cacatttaaa
4021 at
```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42



CGCTCAGGAT...GACTTCCTGCTAGAGATCGGATCCCGGGGCG...ATTATATAGCTCGATCGATCT

TTCTCTTAT...GCGG...ATGGG...TATATACACACAC...GCGGCGGATAGCATGACTGATCTA

CCCATCT...TCT...TTTTCGATACGTCGTC...TTTTCGATACGTCGTC...TTTTCGATACGTCGTC

CACAGACT...ACGGTCTCTACT...ACTTACTAAGCAATTCGGAGAGGGGCGTGGATCGAAGGAG

Nucleotide

My NCBI

[\[Sign In\]](#)

[\[Register\]](#)

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Limits Preview/Index History Clipboard Details

Display ☒ Show ☒ Send to ☒

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [NM_170722](#). Reports Homo sapiens NOD9...[gi:25777609]

[Links](#)

LOCUS NM_170722 3055 bp mRNA linear PRI 10-JUN-2005

DEFINITION Homo sapiens NOD9 protein (NOD9), transcript variant 2, mRNA.

ACCESSION NM_170722

VERSION NM_170722.1 GI:25777609

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3055)

AUTHORS Inohara, N. and Nunez, G.

TITLE NODs: intracellular proteins involved in inflammation and apoptosis

JOURNAL Nat. Rev. Immunol. 3 (5), 371-382 (2003)

PUBMED 12766759

REMARK Review article

COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from [BC013199.1](#) and [BC023974.2](#).

Summary: Alternative splicing has been observed at this gene locus and two transcript variants, encoding distinct isoforms, have been identified. The function of this protein has not been determined.

Transcript Variant: This variant (2) uses an alternate splice site for the 3' terminal exon, resulting in a missing internal segment compared to variant 1. The encoded isoform (2) has a shorter and distinct C-terminus compared to isoform 1.

COMPLETENESS: complete on the 3' end.

FEATURES

Location/Qualifiers

source 1..3055

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/chromosome="11"

/map="11q23.3"

gene 1..3055

/gene="NOD9"

/note="synonyms: FLJ21478, MGC21025"

/db_xref="GeneID:79671"

CDS 240..3005

/gene="NOD9"

/note="isoform 2 is encoded by transcript variant 2"

/codon_start=1

/product="NOD9 protein isoform 2"

/protein_id="NP_733840.1"

/db_xref="GI:25777610"
/db_xref="GeneID:79671"
/translation="MRWGHHLPRASWGSFRRALQRPDDRIPFLIHWSWPLQGERPFG
PPRAFIRHHGSSVDSAPPPGRHGRLFPSASATEAIQRHRRNLAEWFSRLPREERQFGP
TFALDTVHVDPIRESTPDELLRPPAELALEHQPPQAGLPPLALSQLFNPDACGRRVQ
TVVLYGTVGTGKSTLVRKMVLWCYGRLPFELLIPFSCEDLSSLGPAPASLCQLVAQ
RYTPLKEVLPLMAAGSHLLFVLHGLEHLNLDLRLAGTGLCSDPEEPQEPAAIIVNLL
RKYMLPQASILVTTTPSAIGRIPSKYVGRYGEICGFSDTNLQKLYFQLRLNQPYCGYA
VGGSGVSATPAQRDHLVQMLSRNLEGHHQIAAACFLPSYCWLVCATLHFLHAPTAPAGQ
TLTSIYTSFLRLNFSGETLDSTDPSNLSLMAYAARTMGKLAYEGVSSRKTYFSEEDVC
GCLEAGIRTEEEFQLLHIFRRDALRFFLAPCVEPGRAGTFVFTVPAMQEYLAALYIVL
GLRKTTLQKVGKEVAELVGRVGEDVSLVLGIMAKLLPLRALPLLFNLIKVVPRVFGRM
VGKSREAVAQAMVLEMFREEDYYNDDVLDQMGASILGVEGPRRHPDEPPEDEVFELFP
MFMGGLLSAHNRAVLALQGCPIKNLDALENAQAIKKKLGLKGRQVLPPELDDHLFFH
YEFQNRQFSAEVLSSLRQLNLAGVRMTPVKCTVVAVLGSGRHALDEVNLASCQLDPA
GLRTLPLPVFLRARKLGLQLNSLGPEACKDLRLDLLHDQCQITTLRLSNNPLTAAGVAV
LMEGLAGNTSVTHLSLLHTGLGDEGLELLAAQLDRNRQLQELNVAYNGAGDTAALALA
RAAREHPSLELLQGVAIQMCWKPLLLPYAHLWTPRMPSHWCFLILMPPLPQWYDGLV
APRGRCT"
STS 2876..3025
/gene="NOD9"
/standard_name="WI-16056"
/db_xref="UniSTS:53534"
polyA signal 3015..3020
/gene="NOD9"
polyA site 3041
/gene="NOD9"
/experiment="experimental evidence, no additional details
recorded"

ORIGIN

```
1  cgcgggggatg  gaggcaggga  ggggggacga  tggcgggacg  ggtggcgccg  gggttccagc
61  cctgcgcctg  ctccggagca  ccgggcccct  ctcgctgacc  ccctcgcccc  aggaccccg
121  aggcccgagt  gcctgggctc  gtcctctttc  gcgcccgtg  ccaggtgcca  gggccgcgca
181  ggcgggcgga  ggacagaagt  cggtcctagg  cccccaggc  tctgaccttc  tttcccagga
241  tgagggtggg  ccaccatttg  cccagggcct  ctgggggctc  tggttttaga  agagcactcc
301  agcgaccaga  tgatcgatat  cccttcctga  tccactggag  ttggcccttc  caaggggagc
361  gtccctttgg  gccccttagg  gcctttatac  gccaccacgg  aagctcggt  gatagcgctc
421  cccacccctg  gaggcattga  cggctgttcc  ccagcgcttc  tgcaactgaa  gctatacagc
481  ggcaccgccc  gaacctggct  gagggttcca  gccggctgcc  caggaggagg  cgccagtttg
541  gcccacccct  tgccctagac  acggtccacg  ttgaccctgt  gatccgcgag  agtacccttg
601  atgagctact  tcgcccaccc  gcggagctgg  ccctggagca  tcagccaccc  caggccgggc
661  tccccccact  ggccctgtct  cagctcttta  acccggtatg  ctgtgggcgc  cgggtgcaga
721  cagtgggtgct  gtatgggaca  gtgggcacag  gcaagagcac  gctgggtgcg  aagatgggtc
781  tggactgggt  ttatgggcgg  ctgccggcct  tcgagctgct  catccccttc  tcctgtgagg
841  acctgtcatc  cctgggccc  gccccagcct  ccctgtgcc  acttgtggcc  cagcgctaca
901  cgcccctgaa  ggagggttct  cccctgatgg  ctgctgctgg  gtcccacctc  ctctttgtgc
961  tccatggctt  agagcatctc  aacctcgact  tccggctggc  aggcacggga  ctttgtagtg
1021  acccgaggga  accgcaggaa  ccagctgcta  tcctcgctca  cctgctgcgc  aaatacatgc
1081  tgcctcaggc  cagcattctg  gtgaccactc  ggccctctgc  cattggccgt  atcccagca
1141  agtacgtggg  ccgctatggt  gagatctgcg  gtttctctga  taccaacctg  cagaagctct
1201  acttccagct  ccgcctcaac  cagccgtact  gcgggtatgc  cgttggcggt  tcagggtgtc
1261  ctgccacacc  agctcagcgt  gaccacctgg  tgcagatgct  ctcccgaac  ctggaggggc
1321  accaccagat  agccgctgcc  tgcttcctgc  cgtcctattg  ctggctcggt  tgtgccacct
1381  tgcacttctc  gcatgcccc  acgcctgctg  ggcagaccct  tacaagcatc  tataccagct
1441  tcctgcgcct  caacttcagc  ggggaaaccc  tggacagcac  tgaccctcc  aatttgtccc
1501  tgatggccta  tgcagcccga  accatgggca  agttggccta  tgaggggggt  tcctcccgca
1561  agacctactt  ctctgaagag  gatgtctgtg  gctgcctgga  ggctggcatc  aggacggagg
1621  aggagtttca  gctgctgcac  atcttccgtc  gggatgccct  gaggttttcc  ctggcccatc
1681  gtgtggagcc  agggcgtagc  ggcaccttcg  tgttaccgt  gcccgccatg  caggaatacc
1741  tggctgccc  ctacattgtg  ctgggtttgc  gcaagacgac  cctgcaaaag  gtgggcaagg
```

1801 aagtggctga gctcgtgggc cgtgttgggg aggacgtcag cctgggtactg ggcacatcatgg
1861 ccaagctgct gcctctgcgg gctctgcctc tgctcttcaa cctgatcaag gtggttccac
1921 gagtgtttgg gcgcatgggt ggtaaaagcc gggaggcggg ggctcaggcc atggtgctgg
1981 agatgtttcg agaggaggac tactacaacg atgatgttct ggaccagatg ggcgccagta
2041 tcctgggctg ggaggggccc cggcgccacc cagatgagcc ccctgaggat gaagtcttcg
2101 agctcttccc catgttcatg ggggggcttc tctctgccc caaccgagct gtgctagctc
2161 agcttggtg ccccatcaag aacctggatg ccctggagaa tgcccaggcc atcaagaaga
2221 agctgggcaa gctgggcccg caggtgctgc ccccatcaga gctccttgac cacctcttct
2281 tccactatga gttccagaac cagcgttctt ccgctgaggt gctcagctcc ctgcgtcagc
2341 tcaacctggc aggtgtgcgc atgacaccag tcaagtgcac agtgggtggc gctgtgctgg
2401 gcagcggaag gcatgccctg gatgaggtga acttggcctc ctgccagcta gatcctgctg
2461 ggctgcgcac actcctgcct gtcttctctg gtgcccggaa gctgggcttg caactcaaca
2521 gcctgggccc tgaggcctgc aaggacctcc gagacctgtt gctgcatgac cagtgcctaaa
2581 ttaccacact gcggctgtcc aacaaccgc tgacggcggc aggtgttgcc gtgctaattg
2641 aggggctggc aggaaacacc tcagtgcgc acctgtccct gctgcacacg ggccttgggg
2701 acgaaggcct ggagctgctg gctgcccagc tggaccgcaa ccggcagctg caggagctga
2761 acgtggcgta caacggtgct ggtgacacag cggccctggc cctggccaga gctgcccggg
2821 agcacccttc cctggaactg ctacagggtg tcgccatcca gatgtgttg aagcttcccc
2881 tcctgcctta tgctcacctg tggacaccga ggatgcctc acattggtgc tttctcctca
2941 tcctcatgcc ccctttgcca caatggtatg atggcttggt agccctcga ggcagatgca
3001 cctgacttgc tgctattaa aagccgtgtg ccttctacca aaaaaaaaaa aaaaa

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 4 2005 13:52:42



PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Boo

Search for

Limits

Preview/Index

History

Clipboard

Details

 Show:

☐ 1: NT_009325[gi:29746596] This record was removed as a result of standard genome annotation processing. See the genome build documentation at <http://www.ncbi.nlm.nih.gov/genome/guide/build.html> for further information, or contact info@ncbi.nlm.nih.gov.

LOCUS NT_009325 2818927 bp DNA linear CON 10-APR-2003
 DEFINITION Homo sapiens chromosome 11 genomic contig.
 ACCESSION NT_009325
 VERSION NT_009325.14 GI:29746596
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2818927)
 AUTHORS International Human Genome Sequencing Consortium.
 TITLE The DNA sequence of Homo sapiens
 JOURNAL Unpublished (2003)
 COMMENT GENOME ANNOTATION REFSEQ: NCBI contigs are derived from assembled
 genomic sequence data.
 Also see:
Documentation of NCBI's Annotation Process

On Apr 10, 2003 this sequence version replaced gi:27499439.
 This contig has been assembled by NCBI staff from individual clone
 sequences making use of a tiling path supplied by the sequencing
 centers.

COMPLETENESS: not full length.

FEATURES Location/Qualifiers
 source 1..2818927
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="11"
 STS 1256..1453
 /standard_name="SHGC-14206"
 /note="WARNING: map location ambiguous"
 /db_xref="UniSTS:43720"
 gene 1724..2698
 /gene="LOC120806"
 /db_xref="InterimID:120806"
 mRNA 1724..2698
 /gene="LOC120806"
 /product="similar to olfactory receptor MOR40-13 [Mus
 musculus]"
 /note="Derived by automated computational analysis using
 gene prediction method: GenomeScan."
 /transcript_id="XM_062282.7"
 /db_xref="GI:29746563"

```

CDS      /db_xref="InterimID:120806"
         1724..2698
         /gene="LOC120806"
         /codon_start=1
         /protein_id="XP_062282.7"
         /db_xref="GI:29746564"
         /db_xref="InterimID:120806"
STS      6131..6454
         /standard_name="SHGC-147270"
         /db_xref="UniSTS:175711"
gene     19948..20913
         /gene="LOC120807"
         /db_xref="InterimID:120807"
mRNA     19948..20913
         /gene="LOC120807"
         /product="similar to seven transmembrane helix receptor
         [Homo sapiens]"
         /note="Derived by automated computational analysis using
         gene prediction method: GenomeScan."
         /transcript_id="XM_062283.6"
         /db_xref="GI:29746565"
         /db_xref="InterimID:120807"
CDS      19948..20913
         /gene="LOC120807"
         /codon_start=1
         /protein_id="XP_062283.6"
         /db_xref="GI:29746566"
         /db_xref="InterimID:120807"
gene     30369..31256
         /gene="LOC120808"
         /db_xref="InterimID:120808"
mRNA     30369..31256
         /gene="LOC120808"
         /product="similar to seven transmembrane helix receptor
         [Homo sapiens]"
         /note="Derived by automated computational analysis using
         gene prediction method: GenomeScan."
         /transcript_id="XM_062284.5"
         /db_xref="GI:27499400"
         /db_xref="InterimID:120808"
CDS      30369..31256
         /gene="LOC120808"
         /codon_start=1
         /protein_id="XP_062284.5"
         /db_xref="GI:27499401"
         /db_xref="InterimID:120808"
gene     complement(42867..53918)
         /gene="LOC120803"
         /db_xref="InterimID:120803"
mRNA     complement(join(42867..43514,53121..53918))
         /gene="LOC120803"
         /product="similar to seven transmembrane helix receptor
         [Homo sapiens]"
         /note="Derived by automated computational analysis using
         gene prediction method: GenomeScan."
         /transcript_id="XM_062279.6"
         /db_xref="GI:27499402"
         /db_xref="InterimID:120803"
CDS      complement(join(42867..43514,53121..53918))
         /gene="LOC120803"

```

```

/codon_start=1
/protein_id="XP_062279.6"
/db_xref="GI:27499403"
/db_xref="InterimID:120803"
gene 65571..68865
      /gene="LOC253200"
      /db_xref="InterimID:253200"
mRNA join(65571..66030,66338..66511,68747..68865)
      /gene="LOC253200"
      /product="similar to seven transmembrane helix receptor
[Homo sapiens]"
      /note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
      /transcript_id="XM_171485.1"
      /db_xref="GI:22064489"
      /db_xref="InterimID:253200"
CDS join(65571..66030,66338..66511,68747..68865)
      /gene="LOC253200"
      /codon_start=1
      /protein_id="XP_171485.1"
      /db_xref="GI:22064490"
      /db_xref="InterimID:253200"
STS 81037..81232
      /standard_name="D11S2349"
      /note="WARNING: map location ambiguous"
      /db_xref="UniSTS:151812"
gene 85543..100398
      /gene="LOC120800"
      /db_xref="InterimID:120800"
mRNA join(85543..86484,100285..100398)
      /gene="LOC120800"
      /product="similar to seven transmembrane helix receptor
[Homo sapiens]"
      /note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
      /transcript_id="XM_062276.3"
      /db_xref="GI:27499404"
      /db_xref="InterimID:120800"
CDS join(85543..86484,100285..100398)
      /gene="LOC120800"
      /codon_start=1
      /protein_id="XP_062276.3"
      /db_xref="GI:27499405"
      /db_xref="InterimID:120800"
STS 102817..103168
      /standard_name="G54605"
      /note="WARNING: map location ambiguous"
      /db_xref="UniSTS:117740"
STS 102818..103092
      /standard_name="G60067"
      /note="WARNING: map location ambiguous"
      /db_xref="UniSTS:137328"
gene complement(106163..107104)
      /gene="LOC120799"
      /db_xref="InterimID:120799"
mRNA complement(106163..107104)
      /gene="LOC120799"
      /product="similar to Olfactory receptor 52E6"
      /note="Derived by automated computational analysis using
gene prediction method: GenomeScan."

```



```

/ transcript_id="XM_062275.3"
/ db_xref="GI:27499406"
/ db_xref="InterimID:120799"
CDS complement(106163..107104)
/ gene="LOC120799"
/ codon_start=1
/ protein_id="XP_062275.3"
/ db_xref="GI:27499407"
/ db_xref="InterimID:120799"
gene complement(121956..122699)
/ gene="LOC203960"
/ db_xref="InterimID:203960"
mRNA complement(121956..122699)
/ gene="LOC203960"
/ product="similar to Olfactory receptor 52E6"
/ note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/ transcript_id="XM_115089.1"
/ db_xref="GI:20486166"
/ db_xref="InterimID:203960"
CDS complement(121956..122699)
/ gene="LOC203960"
/ codon_start=1
/ protein_id="XP_115089.1"
/ db_xref="GI:20486167"
/ db_xref="InterimID:203960"
gene 139501..140016
/ gene="LOC283290"
/ db_xref="InterimID:283290"
mRNA join(139501..139565,139590..140016)
/ gene="LOC283290"
/ product="similar to olfactory receptor MOR32-1 [Mus
musculus]"
/ note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/ transcript_id="XM_210222.1"
/ db_xref="GI:27499408"
/ db_xref="InterimID:283290"
CDS join(139501..139565,139590..140016)
/ gene="LOC283290"
/ codon_start=1
/ protein_id="XP_210222.1"
/ db_xref="GI:27499409"
/ db_xref="InterimID:283290"
gene 149500..150438
/ gene="LOC283291"
/ db_xref="InterimID:283291"
mRNA 149500..150438
/ gene="LOC283291"
/ product="similar to olfactory receptor MOR32-11 [Mus
musculus]"
/ note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/ transcript_id="XM_210223.1"
/ db_xref="GI:27499410"
/ db_xref="InterimID:283291"
CDS 149500..150438
/ gene="LOC283291"
/ codon_start=1
/ protein_id="XP_210223.1"

```

```

/db_xref="GI:27499411"
/db_xref="InterimID:283291"
gene 155415..213498
      /gene="LOC341274"
      /db_xref="InterimID:341274"
mRNA join(155415..155556,166087..166883,169072..169191,
      193877..194148,209483..209664,212681..213498)
      /gene="LOC341274"
      /product="similar to seven transmembrane helix receptor
      [Homo sapiens]"
      /note="Derived by automated computational analysis using
      gene prediction method: GenomeScan."
      /transcript_id="XM_291976.1"
      /db_xref="GI:29746582"
      /db_xref="InterimID:341274"
CDS join(155415..155556,166087..166883,169072..169191,
      193877..194148,209483..209664,212681..213498)
      /gene="LOC341274"
      /codon_start=1
      /protein_id="XP_291976.1"
      /db_xref="GI:29746583"
      /db_xref="InterimID:341274"
STS 231950..232206
      /standard_name="D11S1338"
      /db_xref="UniSTS:43509"
STS 232004..232203
      /standard_name="D11S1338"
      /db_xref="UniSTS:64797"
gene complement(232757..233575)
      /gene="LOC255723"
      /db_xref="InterimID:255723"
mRNA complement(232757..233575)
      /gene="LOC255723"
      /product="similar to seven transmembrane helix receptor
      [Homo sapiens]"
      /note="Derived by automated computational analysis using
      gene prediction method: GenomeScan."
      /transcript_id="XM_171526.1"
      /db_xref="GI:22066607"
      /db_xref="InterimID:255723"
CDS complement(232757..233575)
      /gene="LOC255723"
      /codon_start=1
      /protein_id="XP_171526.1"
      /db_xref="GI:22066608"
      /db_xref="InterimID:255723"
gene complement(251145..253923)
      /gene="LOC338751"
      /db_xref="InterimID:338751"
mRNA complement(join(251145..252034,253917..253923))
      /gene="LOC338751"
      /product="similar to seven transmembrane helix receptor
      [Homo sapiens]"
      /note="Derived by automated computational analysis using
      gene prediction method: GenomeScan."
      /transcript_id="XM_291977.1"
      /db_xref="GI:29746567"
      /db_xref="InterimID:338751"
CDS complement(join(251145..252034,253917..253923))
      /gene="LOC338751"

```

```

/codon_start=1
/protein_id="XP_291977.1"
/db_xref="GI:29746568"
/db_xref="InterimID:338751"
gene complement(259078..268196)
/gene="LOC120793"
/db_xref="InterimID:120793"
mRNA complement(join(259078..259178,259263..259370,
259509..259974,260199..260364,267259..268196))
/gene="LOC120793"
/product="similar to seven transmembrane helix receptor
[Homo sapiens]"
/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_062269.6"
/db_xref="GI:29746569"
/db_xref="InterimID:120793"
CDS complement(join(259078..259178,259263..259370,
259509..259974,260199..260364,267259..268196))
/gene="LOC120793"
/codon_start=1
/protein_id="XP_062269.6"
/db_xref="GI:29746570"
/db_xref="InterimID:120793"
STS 264685..265010
/standard_name="G63178"
/db_xref="UniSTS:140295"
STS 268806..269035
/standard_name="D11S2415"
/db_xref="UniSTS:71983"
STS 269961..270275
/standard_name="RH123738"
/db_xref="UniSTS:137759"
STS 269961..270273
/standard_name="SHGC-68742"
/db_xref="UniSTS:95528"
gene complement(291952..292896)
/gene="LOC120796"
/db_xref="InterimID:120796"
mRNA complement(291952..292896)
/gene="LOC120796"
/product="similar to seven transmembrane helix receptor
[Homo sapiens]"
/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_062272.7"
/db_xref="GI:29746571"
/db_xref="InterimID:120796"
CDS complement(291952..292896)
/gene="LOC120796"
/codon_start=1
/protein_id="XP_062272.7"
/db_xref="GI:29746572"
/db_xref="InterimID:120796"
gene complement(311166..325389)
/gene="LOC196338"
/db_xref="InterimID:196338"
mRNA complement(join(311166..311751,322524..323379,
325380..325389))
/gene="LOC196338"

```

```

/product="similar to seven transmembrane helix receptor
[Homo sapiens]"
/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_115093.3"
/db_xref="GI:27499418"
/db_xref="InterimID:196338"
CDS      complement(join(311166..311751,322524..323379,
325380..325389))
/gene="LOC196338"
/codon_start=1
/protein_id="XP_115093.3"
/db_xref="GI:27499419"
/db_xref="InterimID:196338"
gene      complement(332017..332996)
/gene="OR52X1P"
/pseudo
/db_xref="LocusID:79272"
misc_feature 348970..535573
/standard_name="RP11-290F24"
/note="FISH-mapped clone"
STS      364652..364866
/standard_name="D11S1241"
/db_xref="UniSTS:148332"
gene      372983..373942
/gene="LOC196335"
/db_xref="InterimID:196335"
mRNA      372983..373942
/gene="LOC196335"
/product="similar to olfactory receptor MOR40-3 [Mus
musculus]"
/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_115092.2"
/db_xref="GI:29746573"
/db_xref="InterimID:196335"
CDS      372983..373942
/gene="LOC196335"
/codon_start=1
/protein_id="XP_115092.1"
/db_xref="GI:20486038"
/db_xref="InterimID:196335"
STS      390560..390830
/standard_name="SHGC-106674"
/db_xref="UniSTS:169983"
misc_feature 392790..520892
/standard_name="RP11-98L18"
/note="FISH-mapped clone"
gene      394045..394700
/gene="LOC120790"
/db_xref="InterimID:120790"
mRNA      join(394045..394447,394666..394700)
/gene="LOC120790"
/product="similar to seven transmembrane helix receptor
[Homo sapiens]"
/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_062266.2"
/db_xref="GI:29746574"
/db_xref="InterimID:120790"

```

CDS join(394045..394447,394666..394700)
 /gene="LOC120790"
 /codon_start=1
 /protein_id="XP_062266.2"
 /db_xref="GI:29746575"
 /db_xref="InterimID:120790"
 STS 396334..396444
 /standard_name="D11S3090"
 /db_xref="UniSTS:152185"
 gene complement(416887..417395)
 /gene="LOC144133"
 /db_xref="InterimID:144133"
 mRNA complement(416887..417395)
 /gene="LOC144133"
 /product="similar to seven transmembrane helix receptor
 [Homo sapiens]"
 /note="Derived by automated computational analysis using
 gene prediction method: BLAST. Supporting evidence
 includes similarity to: 1 mRNA"
 /transcript_id="XM_084743.1"
 /db_xref="GI:18605356"
 /db_xref="InterimID:144133"
 CDS complement(416980..417345)
 /gene="LOC144133"
 /codon_start=1
 /protein_id="XP_084743.1"
 /db_xref="GI:18605357"
 /db_xref="InterimID:144133"
 gene complement(434559..435530)
 /gene="LOC255725"
 /db_xref="InterimID:255725"
 mRNA complement(434559..435530)
 /gene="LOC255725"
 /product="similar to Olfactory receptor 52B2"
 /note="Derived by automated computational analysis using
 gene prediction method: GenomeScan."
 /transcript_id="XM_171528.1"
 /db_xref="GI:22066626"
 /db_xref="InterimID:255725"
 CDS complement(434559..435530)
 /gene="LOC255725"
 /codon_start=1
 /protein_id="XP_171528.1"
 /db_xref="GI:22066627"
 /db_xref="InterimID:255725"
 gene 464428..465390
 /gene="LOC120787"
 /db_xref="InterimID:120787"
 mRNA 464428..465390
 /gene="LOC120787"
 /product="similar to olfactory receptor MOR36-1 [Mus
 musculus]"
 /note="Derived by automated computational analysis using
 gene prediction method: GenomeScan."
 /transcript_id="XM_062263.1"
 /db_xref="GI:17461543"
 /db_xref="InterimID:120787"
 CDS 464428..465390
 /gene="LOC120787"
 /codon_start=1

```

/protein_id="XP_062263.1"
/db_xref="GI:17461544"
/db_xref="InterimID:120787"
STS 467206..467343
/standard_name="G31000"
/db_xref="UniSTS:28049"
gene 470772..476333
/gene="MGC34805"
/db_xref="LocusID:160298"
mRNA join(470772..470891,475054..475852,476116..476333)
/gene="MGC34805"
/product="hypothetical protein MGC34805"
/note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 2 mRNAs"
/transcript_id="NM_173525.1"
/db_xref="GI:27734960"
/db_xref="LocusID:160298"
CDS join(470820..470891,475054..475852,476116..476246)
/gene="MGC34805"
/note="unclassified translation discrepancy"
/codon_start=1
/evidence=not_experimental
/product="hypothetical protein MGC34805"
/protein_id="NP_775796.1"
/db_xref="GI:27734961"
/db_xref="LocusID:160298"
gene complement(476541..499867)
/gene="DKFZP566M1046"
/db_xref="LocusID:84067"
mRNA complement(join(476551..477071,479615..479777,
479937..480115,482575..483354,483762..483967,
484175..484254,487646..487813,488015..488101,
488284..488442,488814..489452,489583..489911,
499748..499849))
/gene="DKFZP566M1046"
/product="hypothetical protein DKFZp566M1046"
/note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 1 mRNA"
/transcript_id="NM_032127.1"
/db_xref="GI:14149782"
/db_xref="LocusID:84067"
CDS complement(join(476710..477071,479615..479777,
479937..480115,482575..483354,483762..483967,
484175..484254,487646..487813,488015..488101,
488284..488442,488814..489452,489583..489720))
/gene="DKFZP566M1046"
/note="similarity to C.elegans C05D11.8; unclassified
translation discrepancy"
/codon_start=1
/product="hypothetical protein DKFZp566M1046"
/protein_id="NP_115503.1"
/db_xref="GI:14149783"
/db_xref="LocusID:84067"
STS 480870..481044
/standard_name="G20710;A006C42"
/db_xref="UniSTS:68786"

```

```

STS      /db_xref="UniSTS:68787"
         491270..491403
         /standard_name="D11S4412"
         /db_xref="UniSTS:54740"
gene     500098..509681
         /gene="LOC338753"
         /db_xref="InterimID:338753"
mRNA     join(500098..500213,504588..504689,504888..504994,
         505270..505915,506635..509681)
         /gene="LOC338753"
         /product="similar to Cyclic nucleotide gated cation
         channel; olfactory cyclic nucleotide-gated channel [Rattus
         norvegicus]"
         /note="Derived by automated computational analysis using
         gene prediction method: BLAST. Supporting evidence
         includes similarity to: 1 mRNA"
         /transcript_id="XM_290552.1"
         /db_xref="GI:29746576"
CDS      /db_xref="InterimID:338753"
         join(504646..504689,504888..504994,505270..505915,
         506635..507088)
         /gene="LOC338753"
         /codon_start=1
         /protein_id="XP_290552.1"
         /db_xref="GI:29746577"
         /db_xref="InterimID:338753"
misc_feature 520658..520892
         /standard_name="RP11-645I8"
         /note="FISH-mapped clone"
misc_feature 520658..520791
         /standard_name="RP11-149K16"
         /note="FISH-mapped clone"
STS      520658..520791
         /standard_name="D11S1323"
         /db_xref="UniSTS:67612"
STS      520688..520892
         /standard_name="D11S1323"
         /db_xref="UniSTS:72457"
STS      522183..522469
         /standard_name="SHGC-111644"
         /db_xref="UniSTS:168453"
gene     524947..537329
         /gene="CCKBR"
         /db_xref="LocusID:887"
         /db_xref="MIM:118445"
mRNA     join(525130..525283,534873..535124,535292..535541,
         535850..537329)
         /gene="CCKBR"
         /product="cholecystokinin B receptor"
         /note="unclassified transcription discrepancy; Derived by
         automated computational analysis using gene prediction
         method: BestRefseq,BLAST. Supporting evidence includes
         similarity to: 1 mRNA"
         /transcript_id="NM_000731.2"
         /db_xref="GI:21361152"
         /db_xref="LocusID:887"
         /db_xref="MIM:118445"
CDS      join(525133..525283,534873..535124,535292..535541,
         535850..536747)
         /gene="CCKBR"

```

```

/feature
  STS
    /note="unclassified translation discrepancy"
    /codon_start=1
    /product="cholecystokinin B receptor"
    /protein_id="NP_000722.2"
    /db_xref="GI:21361153"
    /db_xref="LocusID:887"
    /db_xref="MIM:118445"
    537249..537459
    /standard_name="RH69002"
    /db_xref="UniSTS:66177"
  misc_feature
    557896..718429
    /standard_name="RP11-30I3"
    /note="FISH-mapped clone"
  gene
    complement(584152..585851)
    /gene="PRKCDBP"
    /db_xref="LocusID:112464"
  mRNA
    complement(join(584152..584768,585297..585714))
    /gene="PRKCDBP"
    /product="protein kinase C, delta binding protein"
    /note="unclassified transcription discrepancy; Derived by
    automated computational analysis using gene prediction
    method: BestRefseq,BLAST. Supporting evidence includes
    similarity to: 1 mRNA"
    /transcript_id="NM_145040.1"
    /db_xref="GI:21450786"
    /db_xref="LocusID:112464"
  STS
    584152..584391
    /standard_name="RH80357"
    /db_xref="UniSTS:87546"
  STS
    584165..584299
    /standard_name="RH103676"
    /db_xref="UniSTS:98001"
  STS
    584264..584407
    /standard_name="STS-AA030008"
    /db_xref="UniSTS:58285"
  CDS
    complement(join(584367..584768,585297..585680))
    /gene="PRKCDBP"
    /note="unclassified translation discrepancy"
    /codon_start=1
    /product="protein kinase C, delta binding protein"
    /protein_id="NP_659477.1"
    /db_xref="GI:21450787"
    /db_xref="LocusID:112464"
  gene
    589235..645662
    /gene="LOC341275"
    /db_xref="InterimID:341275"
  mRNA
    join(589235..589239,594769..594837,598041..598102,
    628274..628491,645432..645662)
    /gene="LOC341275"
    /product="LOC341275"
    /note="Derived by automated computational analysis using
    gene prediction method: GenomeScan."
    /transcript_id="XM_296082.1"
    /db_xref="GI:29746584"
    /db_xref="InterimID:341275"
  CDS
    join(589235..589239,594769..594837,598041..598102,
    628274..628491,645432..645662)
    /gene="LOC341275"
    /codon_start=1
    /protein_id="XP_296082.1"

```



```

/db_xref="GI:29746585"
/db_xref="InterimID:341275"
STS 600036..600175
     /gene="LOC341275"
     /standard_name="RH92838"
     /db_xref="UniSTS:85687"
STS 602093..602296
     /gene="LOC341275"
     /standard_name="D11S1997"
     /db_xref="UniSTS:82667"
STS 609826..609949
     /gene="LOC341275"
     /standard_name="RH92043"
     /db_xref="UniSTS:85957"
STS 610489..610663
     /gene="LOC341275"
     /standard_name="D11S4034"
     /db_xref="UniSTS:21496"
misc_feature 654687..655117
             /standard_name="RP11-93A12"
             /note="FISH-mapped clone"
gene 655536..660199
     /gene="SMPD1"
     /db_xref="LocusID:6609"
     /db_xref="MIM:257200"
STS 655762..655958
     /gene="SMPD1"
     /standard_name="STS-M81780"
     /db_xref="UniSTS:12276"
mRNA join(655803..656120,656588..657360,658420..658591,
        658821..658897,659100..659245,659402..659811)
     /gene="SMPD1"
     /product="sphingomyelin phosphodiesterase 1, acid
lysosomal (acid sphingomyelinase)"
     /note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 1 mRNA"
     /transcript_id="NM_000543.1"
     /db_xref="GI:4507092"
     /db_xref="LocusID:6609"
     /db_xref="MIM:257200"
CDS join(655803..656120,656588..657360,658420..658591,
        658821..658897,659100..659245,659402..659805)
     /gene="SMPD1"
     /EC_number="3.1.4.12"
     /note="unclassified translation discrepancy; sphingomyelin
phosphodiesterase-1, acid lysosomal"
     /codon_start=1
     /product="sphingomyelin phosphodiesterase 1, acid
lysosomal (acid sphingom"
     /protein_id="NP_000534.1"
     /db_xref="GI:4507093"
     /db_xref="LocusID:6609"
     /db_xref="MIM:257200"
STS 656338..656505
     /gene="SMPD1"
     /standard_name="RH69187"
     /db_xref="UniSTS:66320"
STS 659827..660152

```

```

/ gene="SMPD1"
/ standard_name="D11S4426"
/ db_xref="UniSTS:21687"
STS      659864..660075
/ gene="SMPD1"
/ standard_name="SMPD1"
/ db_xref="UniSTS:48627"
gene      complement(660329..684618)
/ gene="APBB1"
/ db_xref="LocusID:322"
/ db_xref="MIM:602709"
mRNA      complement(join(660329..660905,660990..661166,
661304..661419,666193..666276,666549..666633,
666778..666892,667286..667413,667780..667929,
668349..668412,668523..668608,668692..668748,
668851..669026,675831..676565,684550..684618))
/ gene="APBB1"
/ product="amyloid beta (A4) precursor protein-binding,
family B, member 1 (Fe65)"
/ note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 4 mRNAs"
/ transcript_id="NM_145689.1"
/ db_xref="GI:22035553"
/ db_xref="LocusID:322"
/ db_xref="MIM:602709"
mRNA      complement(join(660329..660905,660990..661166,
661304..661419,666193..666276,666549..666633,
666778..666892,667283..667413,667780..667929,
668349..668412,668523..668608,668692..668748,
668851..669026,675831..676565,684189..684274))
/ gene="APBB1"
/ product="amyloid beta (A4) precursor protein-binding,
family B, member 1 (Fe65)"
/ note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 1 mRNA"
/ transcript_id="NM_001164.2"
/ db_xref="GI:22035552"
/ db_xref="LocusID:322"
/ db_xref="MIM:602709"
STS      660354..660566
/ standard_name="A002D29"
/ db_xref="UniSTS:17869"
CDS      complement(join(660738..660905,660990..661166,
661304..661419,666193..666276,666549..666633,
666778..666892,667286..667413,667780..667929,
668349..668412,668523..668608,668692..668748,
668851..669026,675831..676551))
/ gene="APBB1"
/ note="amyloid beta A4 precursor protein-binding, family
B, member 1; stat-like protein; adaptor protein FE65a2"
/ codon_start=1
/ product="amyloid beta A4 precursor protein-binding,
family B, member 1 isoform delta E9"
/ protein_id="NP_663722.1"
/ db_xref="GI:22035554"
/ db_xref="LocusID:322"

```

CDS /db_xref="MIM:602709"
 complement(join(660738..660905;660990..661166,
 661304..661419,666193..666276,666549..666633,
 666778..666892,667283..667413,667780..667929,
 668349..668412,668523..668608,668692..668748,
 668851..669026,675831..676551))
 /gene="APBB1"
 /note="unclassified translation discrepancy; amyloid beta
 A4 precursor protein-binding, family B, member 1;
 stat-like protein; adaptor protein FE65a2"
 /codon_start=1
 /product="amyloid beta A4 precursor protein-binding,
 family B, member 1 isoform E9"
 /protein_id="NP_001155.1"
 /db_xref="GI:4502131"
 /db_xref="LocusID:322"
 /db_xref="MIM:602709"
 STS 665795..665910
 /standard_name="G63687"
 /db_xref="UniSTS:140649"
 gene complement(696255..707790)
 /gene="HPX"
 /db_xref="LocusID:3263"
 /db_xref="MIM:142290"
 STS 696285..696407
 /standard_name="D11S4588"
 /db_xref="UniSTS:68264"
 mRNA complement(join(696415..696674,696845..697007,
 697091..697221,702249..702380,702643..702855,
 703559..703712,705368..705489,705670..705741,
 705863..705921,706072..706154))
 /gene="HPX"
 /product="hemopexin"
 /note="Derived by automated computational analysis using
 gene prediction method: BestRefseq,BLAST. Supporting
 evidence includes similarity to: 1 mRNA"
 /transcript_id="NM_000613.1"
 /db_xref="GI:11321560"
 /db_xref="LocusID:3263"
 /db_xref="MIM:142290"
 CDS complement(join(696415..696674,696845..697007,
 697091..697221,702249..702380,702643..702855,
 703559..703712,705368..705489,705670..705741,
 705863..705921,706072..706154))
 /gene="HPX"
 /note="precursor"
 /codon_start=1
 /product="hemopexin"
 /protein_id="NP_000604.1"
 /db_xref="GI:11321561"
 /db_xref="LocusID:3263"
 /db_xref="MIM:142290"
 STS 705708..706162
 /standard_name="GDB:197845"
 /db_xref="UniSTS:155963"
 gene complement(713807..739180)
 /gene="TRIM3"
 /db_xref="LocusID:10612"
 /db_xref="MIM:605493"
 STS 713826..714010

```

/standard_name="RH71141"
/db_xref="UniSTS:60910"
STS 713826..713961
/standard_name="RH47384"
/db_xref="UniSTS:60909"
STS 713826..713953
/standard_name="SGC34546"
/db_xref="UniSTS:60911"
mRNA complement(join(714196..714373,714499..714639,
715744..715814,716085..716253,716464..716631,
721265..721368,721490..722014,722518..722669,
722889..723040,723258..723489,730758..730888))
/gene="TRIM3"
/product="tripartite motif-containing 3"
/note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 1 mRNA"
/transcript_id="NM_033279.1"
/db_xref="GI:15451754"
/db_xref="LocusID:10612"
/db_xref="MIM:605493"
mRNA complement(join(714196..714373,714499..714639,
715744..715814,716085..716253,716464..716631,
721265..721368,721490..722222,722489..722669,
722889..723040,723258..723489,730758..730888))
/gene="TRIM3"
/product="tripartite motif-containing 3"
/note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 2 mRNAs"
/transcript_id="NM_006458.1"
/db_xref="GI:5453568"
/db_xref="LocusID:10612"
/db_xref="MIM:605493"
CDS complement(join(714221..714373,714499..714639,
715744..715814,716085..716253,716464..716631,
721265..721368,721490..722014,722518..722669,
722889..723040,723258..723489,730758..730888))
/gene="TRIM3"
/note="unclassified translation discrepancy; brain
expressed ring finger; tripartite motif protein TRIM3;
ring finger protein 22"
/codon_start=1
/product="tripartite motif-containing 3 isoform gamma"
/protein_id="NP_150595.1"
/db_xref="GI:15451755"
/db_xref="LocusID:10612"
/db_xref="MIM:605493"
CDS complement(join(714221..714373,714499..714639,
715744..715814,716085..716253,716464..716631,
721265..721368,721490..722222,722489..722669,
722889..723040,723258..723489,730758..730888))
/gene="TRIM3"
/note="unclassified translation discrepancy; brain
expressed ring finger; tripartite motif protein TRIM3"
/codon_start=1
/product="ring finger protein 22, isoform alpha"
/protein_id="NP_006449.1"

```

```

/db_xref="GI:5453569"
/db_xref="LocusID:10612"
/db_xref="MIM:605493"
STS 721548..721721
     /standard_name="RH12618"
     /db_xref="UniSTS:89873"
STS 733994..734146
     /standard_name="D11S4905"
     /db_xref="UniSTS:76599"
STS 735340..735489
     /standard_name="D11S2391"
     /db_xref="UniSTS:50314"
STS 735357..735483
     /standard_name="RH91168"
     /db_xref="UniSTS:85551"
STS 735367..735479
     /standard_name="D11S2266E"
     /db_xref="UniSTS:46848"
STS 735378..735501
     /standard_name="SHGC-30684"
     /db_xref="UniSTS:6728"
STS 739925..740175
     /standard_name="WI-22461"
     /db_xref="UniSTS:48639"
STS 739926..739997
     /standard_name="STS-Z40796"
     /db_xref="UniSTS:31171"
STS 741731..741920
     /standard_name="IB2126"
     /db_xref="UniSTS:78484"
gene complement(741745..746532)
     /gene="POR1"
     /db_xref="LocusID:23647"
     /db_xref="MIM:601638"
mRNA complement(join(741745..742461,742911..743085,
743234..743391,743931..744152,744333..744451,
745165..745261,745516..745616,746424..746488))
     /gene="POR1"
     /product="partner of RAC1 (arfaptin 2)"
     /note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 1 mRNA"
     /transcript_id="NM_012402.1"
     /db_xref="GI:6912601"
     /db_xref="LocusID:23647"
     /db_xref="MIM:601638"
STS 741770..741897
     /standard_name="RH11646"
     /db_xref="UniSTS:23650"
CDS complement(join(742306..742461,742911..743085,
743234..743391,743931..744152,744333..744451,
745165..745261,745516..745614))
     /gene="POR1"
     /codon_start=1
     /product="partner of RAC1 (arfaptin 2)"
     /protein_id="NP_036534.1"
     /db_xref="GI:6912602"
     /db_xref="LocusID:23647"
     /db_xref="MIM:601638"

```

```

gene      746656..749873
          /gene="FXC1"
          /db_xref="LocusID:26515"
          /db_xref="MIM:607388"
mRNA      join(746656..746748,746950..747045,747238..748514)
          /gene="FXC1"
          /product="fracture callus 1 homolog (rat)"
          /note="unclassified transcription discrepancy; Derived by
          automated computational analysis using gene prediction
          method: BestRefseq, BLAST. Supporting evidence includes
          similarity to: 6 mRNAs"
          /transcript_id="NM_012192.1"
          /db_xref="GI:6912381"
          /db_xref="LocusID:26515"
          /db_xref="MIM:607388"
CDS       join(746711..746748,746950..747045,747238..747414)
          /gene="FXC1"
          /note="putatively involved in mitochondrial carrier import
          into the inner membrane; similar to yeast Tim9; similar to
          the Tim10/Tim12/DDP protein family; unclassified
          translation discrepancy; fracture callus 1 (rat) homolog"
          /codon_start=1
          /product="fracture callus 1 homolog"
          /protein_id="NP_036324.1"
          /db_xref="GI:6912382"
          /db_xref="LocusID:26515"
          /db_xref="MIM:607388"
STS       748047..748189
          /gene="FXC1"
          /standard_name="RH103170"
          /db_xref="UniSTS:97503"
STS       756313..756411
          /standard_name="SHGC-57652"
          /db_xref="UniSTS:53802"
misc_feature 760537..929997
          /standard_name="RP11-8906"
          /note="FISH-mapped clone"
gene      762453..769393
          /gene="LOC283293"
          /db_xref="InterimID:283293"
mRNA      join(762453..762524,762778..762860,763916..764154,
          767946..769393)
          /gene="LOC283293"
          /product="LOC283293"
          /note="Derived by automated computational analysis using
          gene prediction method: BLAST. Supporting evidence
          includes similarity to: 1 mRNA"
          /transcript_id="XM_210962.1"
          /db_xref="GI:27499422"
          /db_xref="InterimID:283293"
CDS       768095..768391
          /gene="LOC283293"
          /codon_start=1
          /protein_id="XP_210962.1"
          /db_xref="GI:27499423"
          /db_xref="InterimID:283293"
gene      773406..786051
          /gene="FLJ35709"
          /db_xref="LocusID:283294"
mRNA      join(773406..774276,774355..774465,776466..776622,

```

```

784793..785047,785158..786051)
/gene="FLJ35709"
/product="hypothetical protein FLJ35709"
/note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 2 mRNAs"
/transcript_id="NM_173589.1"
/db_xref="GI:27734792"
/db_xref="LocusID:283294"
CDS
join(774086..774276,774355..774465,776466..776622,
784793..785047,785158..785304)
/gene="FLJ35709"
/codon_start=1
/evidence=not_experimental
/product="hypothetical protein FLJ35709"
/protein_id="NP_775860.1"
/db_xref="GI:27734793"
/db_xref="LocusID:283294"
STS
791393..791637
/standard_name="D11S4585"
/db_xref="UniSTS:34466"
gene
799117..814228
/gene="LOC196337"
/db_xref="InterimID:196337"
mRNA
join(799117..799422,803576..803703,803805..804003,
804412..804506,805069..805276,809314..809439,
809767..809864,810070..812859,813056..813595,
813838..814228)
/gene="LOC196337"
/product="similar to FLJ00251 protein [Homo sapiens]"
/note="Derived by automated computational analysis using
gene prediction method: BLAST. Supporting evidence
includes similarity to: 2 mRNAs"
/transcript_id="XM_113696.1"
/db_xref="GI:20486053"
/db_xref="InterimID:196337"
CDS
join(810159..812859,813056..813273)
/gene="LOC196337"
/codon_start=1
/protein_id="XP_113696.1"
/db_xref="GI:20486054"
/db_xref="InterimID:196337"
STS
814086..814210
/gene="LOC196337"
/standard_name="WI-11771"
/db_xref="UniSTS:79547"
STS
814885..815009
/standard_name="WI-14280"
/db_xref="UniSTS:63605"
gene
829630..837212
/gene="FLJ32752"
/db_xref="LocusID:144132"
mRNA
join(831298..831586,831780..831958,832088..833053,
833249..833435,833647..833769,833858..834059,
835202..835293,835440..835589,835811..836616,
836829..837212)
/gene="FLJ32752"
/product="hypothetical protein FLJ32752"
/note="unclassified transcription discrepancy; Derived by

```

automated computational analysis using gene prediction
 method: BestRefseq,BLAST. Supporting evidence includes
 similarity to: 1 mRNA
 /transcript_id="NM_144666.1"
 /db_xref="GI:21389554"
 /db_xref="LocusID:144132"
 CDS join(831577..831586,831780..831958,832088..833053,
 833249..833435,833647..833769,833858..834059,
 835202..835293,835440..835589,835811..836616,
 836829..837179)
 /gene="FLJ32752"
 /codon_start=1
 /evidence=not_experimental
 /product="hypothetical protein FLJ32752"
 /protein_id="NP_653267.1"
 /db_xref="GI:21389555"
 /db_xref="LocusID:144132"
 STS 836965..837149
 /gene="FLJ32752"
 /standard_name="RH99124"
 /db_xref="UniSTS:87363"
 STS 853653..853781
 /standard_name="WI-17590"
 /db_xref="UniSTS:36616"
 gene complement(857572..860245)
 /gene="LOC283295"
 /db_xref="InterimID:283295"
 mRNA complement(857572..860245)
 /gene="LOC283295"
 /product="LOC283295"
 /note="Derived by automated computational analysis using
 gene prediction method: BLAST. Supporting evidence
 includes similarity to: 1 mRNA"
 /transcript_id="XM_210964.1"
 /db_xref="GI:27499426"
 /db_xref="InterimID:283295"
 STS 859321..859457
 /standard_name="D11S4708"
 /db_xref="UniSTS:21088"
 CDS complement(859657..859944)
 /gene="LOC283295"
 /codon_start=1
 /protein_id="XP_210964.1"
 /db_xref="GI:27499427"
 /db_xref="InterimID:283295"
 gene complement(860268..868789)
 /gene="KIAA0409"
 /db_xref="LocusID:23378"
 mRNA complement(join(865117..865458,865679..865775,
 865862..865968,866119..866248,866342..866795,
 867045..867408,868597..868774))
 /gene="KIAA0409"
 /product="KIAA0409 protein"
 /note="unclassified transcription discrepancy; Derived by
 automated computational analysis using gene prediction
 method: BestRefseq,BLAST. Supporting evidence includes
 similarity to: 1 mRNA"
 /transcript_id="NM_015324.1"
 /db_xref="GI:12758124"
 /db_xref="LocusID:23378"


```

STS      865126..865257
         /standard_name="WI-15843"
         /db_xref="UniSTS:3340"
STS      865136..865235
         /standard_name="G59726"
         /db_xref="UniSTS:137024"
STS      865146..865286
         /standard_name="RH47197"
         /db_xref="UniSTS:39346"
STS      865151..865287
         /standard_name="A007B37"
         /db_xref="UniSTS:16348"
CDS      complement(join(865339..865458,865679..865775,
         865862..865968,866119..866248,866342..866795,
         867045..867408,868597..868695))
         /gene="KIAA0409"
         /note="unclassified translation discrepancy"
         /codon_start=1
         /evidence=not_experimental
         /product="KIAA0409 protein"
         /protein_id="NP_056139.1"
         /db_xref="GI:12758125"
         /db_xref="LocusID:23378"
STS      867136..867260
         /standard_name="WI-12713"
         /db_xref="UniSTS:10454"
gene     868947..876060
         /gene="ILK"
         /db_xref="LocusID:3611"
         /db_xref="MIM:602366"
mRNA     join(868975..869015,869373..869553,873235..873400,
         873583..873678,873883..873979,874073..874156,
         874260..874345,874488..874597,874701..874828,
         874913..875034,875125..875224,875337..875467,
         875651..876055)
         /gene="ILK"
         /product="integrin-linked kinase"
         /note="unclassified transcription discrepancy; Derived by
         automated computational analysis using gene prediction
         method: BestRefseq,BLAST. Supporting evidence includes
         similarity to: 1 mRNA"
         /transcript_id="NM_004517.1"
         /db_xref="GI:4758605"
         /db_xref="LocusID:3611"
         /db_xref="MIM:602366"
CDS      join(869465..869553,873235..873400,873583..873678,
         873883..873979,874073..874156,874260..874345,
         874488..874597,874701..874828,874913..875034,
         875125..875224,875337..875467,875651..875800)
         /gene="ILK"
         /function="protein serine/threonine kinase"
         /codon_start=1
         /product="integrin-linked kinase"
         /protein_id="NP_004508.1"
         /db_xref="GI:4758606"
         /db_xref="LocusID:3611"
         /db_xref="MIM:602366"
gene     complement(871489..877403)
         /gene="TAF10"
         /db_xref="LocusID:6881"

```

```

      /db_xref="MIM:600475"
STS      872508..872782
      /gene="ILK"
      /standard_name="WI-22555"
      /db_xref="UniSTS:5777"
STS      873528..873781
      /gene="ILK"
      /standard_name="RH12375"
      /db_xref="UniSTS:23970"
STS      875771..875992
      /gene="ILK"
      /standard_name="A002C40"
      /db_xref="UniSTS:5081"
mRNA      complement(join(876031..876200,876378..876492,
      876577..876641,876853..877007,877147..877403))
      /gene="TAF10"
      /product="TAF10 RNA polymerase II, TATA box binding
      protein (TBP)-associated factor, 30kDa"
      /note="Derived by automated computational analysis using
      gene prediction method: BestRefseq,BLAST. Supporting
      evidence includes similarity to: 1 mRNA"
      /transcript_id="NM_006284.2"
      /db_xref="GI:21166374"
      /db_xref="LocusID:6881"
      /db_xref="MIM:600475"
CDS      complement(join(876111..876200,876378..876492,
      876577..876641,876853..877007,877147..877378))
      /gene="TAF10"
      /note="TATA box binding protein (TBP)-associated factor,
      RNA polymerase II; TAF10 RNA polymerase II, TATA box
      binding protein (TBP)-associated factor, 30 kD; TATA box
      binding protein (TBP)-associated factor, RNA polymerase
      II, H, 30kD; transcription initiation factor TFIID 30 kD
      subunit"
      /codon_start=1
      /product="TBP-related factor 10"
      /protein_id="NP_006275.1"
      /db_xref="GI:5454106"
      /db_xref="LocusID:6881"
      /db_xref="MIM:600475"
STS      876607..876733
      /standard_name="RH70892"
      /db_xref="UniSTS:35021"
gene      complement(877958..884618)
      /gene="CLN2"
      /db_xref="LocusID:1200"
      /db_xref="MIM:204500"
mRNA      complement(join(877958..879875,880055..880180,
      880360..880518,880631..880751,881194..881263,
      881504..881692,881849..882047,882163..882341,
      882489..882616,882815..882965,883965..884104,
      884385..884456,884573..884618))
      /gene="CLN2"
      /product="ceroid-lipofuscinosis, neuronal 2, late
      infantile (Jansky-Bielschowsky disease)"
      /note="unclassified transcription discrepancy; Derived by
      automated computational analysis using gene prediction
      method: BestRefseq,BLAST. Supporting evidence includes
      similarity to: 1 mRNA"
      /transcript_id="NM_000391.2"

```

```

/db_xref="GI:5597012"
/db_xref="LocusID:1200"
/db_xref="MIM:204500"
STS      877967..878092
         /standard_name="WI-11808"
         /db_xref="UniSTS:12935"
STS      879026..879140
         /standard_name="RH36325"
         /db_xref="UniSTS:18215"
CDS      complement(join(879735..879875,880055..880180,
880360..880518,880631..880751,881194..881263,
881504..881692,881849..882047,882163..882341,
882489..882616,882815..882965,883965..884104,
884385..884456,884573..884589))
         /gene="CLN2"
         /note="deficient in late-infantile neuronal ceroid
lipofuscinosis; unclassified translation discrepancy"
         /codon_start=1
         /product="ceroid-lipofuscinosis, neuronal 2, late
infantile (Jansky-Bielschowsky disease)"
         /protein_id="NP_000382.3"
         /db_xref="GI:5729770"
         /db_xref="LocusID:1200"
         /db_xref="MIM:204500"
STS      884275..884387
         /standard_name="D11S3007"
         /db_xref="UniSTS:152113"
gene     complement(886517..921034)
         /gene="PCDH16"
         /db_xref="LocusID:8642"
         /db_xref="MIM:603057"
mRNA     complement(join(886517..889580,889920..890058,
890388..890671,890787..890917,891110..891264,
891359..891570,891742..891855,891979..892857,
893811..894020,894642..894767,894862..895101,
895189..896053,896243..896400,896501..896597,
896806..896999,897221..898246,898602..898838,
898979..899210,899308..899496,905008..906924,
920754..920815))
         /gene="PCDH16"
         /product="protocadherin 16 dachshous-like (Drosophila)"
         /note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 1 mRNA"
         /transcript_id="NM_003737.1"
         /db_xref="GI:16933556"
         /db_xref="LocusID:8642"
         /db_xref="MIM:603057"
STS      886610..886776
         /standard_name="RH94204"
         /db_xref="UniSTS:88555"
CDS      complement(join(886969..889580,889920..890058,
890388..890671,890787..890917,891110..891264,
891359..891570,891742..891855,891979..892857,
893811..894020,894642..894767,894862..895101,
895189..896053,896243..896400,896501..896597,
896806..896999,897221..898246,898602..898838,
898979..899210,899308..899496,905008..906804))
         /gene="PCDH16"

```

```

/note="unclassified translation discrepancy; protocadherin
16; fibroblast cadherin FIB1; fibroblast cadherin 1;
dachsaus homologue; cadherin related 25, dachsaus
(Drosophila) homolog"
/codon_start=1
/product="protocadherin 16 precursor"
/protein_id="NP_003728.1"
/db_xref="GI:16933557"
/db_xref="LocusID:8642"
/db_xref="MIM:603057"
STS      899445..899663
          /standard_name="SHGC-141500"
          /db_xref="UniSTS:182384"
STS      929631..929964
          /standard_name="RH119121"
          /db_xref="UniSTS:139013"
STS      945961..946201
          /standard_name="STS-AA039615"
          /db_xref="UniSTS:76931"
STS      946151..946322
          /standard_name="RH98881"
          /db_xref="UniSTS:90197"
gene      complement(946344..948534)
          /gene="MRPL17"
          /db_xref="LocusID:63875"
mRNA      complement(join(946840..947593,947938..948006,
          948314..948534))
          /gene="MRPL17"
          /product="mitochondrial ribosomal protein L17"
          /note="Derived by automated computational analysis using
          gene prediction method: BestRefseq,BLAST. Supporting
          evidence includes similarity to: 2 mRNAs"
          /transcript_id="NM_022061.2"
          /db_xref="GI:27477130"
          /db_xref="LocusID:63875"
STS      947160..947309
          /standard_name="SGC33125"
          /db_xref="UniSTS:44831"
STS      947182..947334
          /standard_name="RH41797"
          /db_xref="UniSTS:7445"
CDS      complement(join(947309..947593,947938..948006,
          948314..948487))
          /gene="MRPL17"
          /note="LYST-interacting protein LIP2"
          /codon_start=1
          /product="mitochondrial ribosomal protein L17"
          /protein_id="NP_071344.1"
          /db_xref="GI:11596859"
          /db_xref="LocusID:63875"
STS      947312..947496
          /standard_name="STS-T56255"
          /db_xref="UniSTS:5803"
STS      951373..951501
          /standard_name="SGC30555"
          /db_xref="UniSTS:62906"
STS      971066..971225
          /standard_name="WI-3891"
          /db_xref="UniSTS:76898"
STS      973547..973821

```

```

/standard_name="SHGC-132044"
/db_xref="UniSTS:173888"
STS 973688..973837
/standard_name="SHGC-1124"
/db_xref="UniSTS:11419"
gene complement(978343..981721)
/ gene="FLJ13373"
/db_xref="LocusID:80073"
mRNA complement(979531..981655)
/ gene="FLJ13373"
/ product="hypothetical protein FLJ13373"
/ note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 1. mRNA"
/ transcript_id="NM_025006.1"
/db_xref="GI:13376522"
/db_xref="LocusID:80073"
CDS complement(979802..981190)
/ gene="FLJ13373"
/ note="unclassified translation discrepancy"
/ codon_start=1
/ evidence=not_experimental
/ product="hypothetical protein FLJ13373"
/ protein_id="NP_079282.1"
/db_xref="GI:13376523"
/db_xref="LocusID:80073"
STS 986433..986624
/standard_name="RH120124"
/db_xref="UniSTS:132329"
STS 1003372..1003669
/standard_name="SHGC-84480"
/db_xref="UniSTS:102832"
STS 1005382..1005702
/standard_name="SHGC-111926"
/db_xref="UniSTS:182361"
gene complement(1008603..1011650)
/ gene="LOC283296"
/db_xref="InterimID:283296"
mRNA complement(1008603..1011650)
/ gene="LOC283296"
/ product="LOC283296"
/ note="Derived by automated computational analysis using
gene prediction method: BLAST. Supporting evidence
includes similarity to: 1 mRNA"
/ transcript_id="XM_210966.1"
/db_xref="GI:27499428"
/db_xref="InterimID:283296"
CDS complement(1010888..1011364)
/ gene="LOC283296"
/ codon_start=1
/ protein_id="XP_210966.1"
/db_xref="GI:27499429"
/db_xref="InterimID:283296"
gene 1014396..1015224
/ gene="LOC338754"
/db_xref="InterimID:338754"
mRNA join(1014396..1014536,1014937..1015224)
/ gene="LOC338754"
/ product="similar to hypothetical protein FLJ13373 [Homo

```

```

sapiens]"
/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_291979.1"
/db_xref="GI:29746578"
/db_xref="InterimID:338754"
CDS
join(1014396..1014536,1014937..1015224)
/gene="LOC338754"
/codon_start=1
/protein_id="XP_291979.1"
/db_xref="GI:29746579"
/db_xref="InterimID:338754"
STS
1015393..1015518
/standard_name="D11S2706"
/db_xref="UniSTS:151929"
gene
complement(1033198..1034148)
/gene="LOC338755"
/db_xref="InterimID:338755"
mRNA
complement(1033198..1034148)
/gene="LOC338755"
/product="similar to Olfactory receptor 2AG1 (HT3)"
/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_291980.1"
/db_xref="GI:29746580"
/db_xref="InterimID:338755"
CDS
complement(1033198..1034148)
/gene="LOC338755"
/codon_start=1
/protein_id="XP_291980.1"
/db_xref="GI:29746581"
/db_xref="InterimID:338755"
misc_feature
1034664..1208274
/standard_name="RP11-560B16"
/note="FISH-mapped clone"
gene
1050199..1051149
/gene="LOC144125"
/db_xref="InterimID:144125"
mRNA
1050199..1051149
/gene="LOC144125"
/product="similar to Olfactory receptor 2AG1 (HT3)"
/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_090203.1"
/db_xref="GI:18605333"
/db_xref="InterimID:144125"
CDS
1050199..1051149
/gene="LOC144125"
/codon_start=1
/protein_id="XP_090203.1"
/db_xref="GI:18605334"
/db_xref="InterimID:144125"
gene
complement(1059885..1060868)
/gene="OR6A1"
/db_xref="LocusID:8590"
mRNA
complement(1059885..1060868)
/gene="OR6A1"
/product="olfactory receptor, family 6, subfamily A,
member 1"
/note="unclassified transcription discrepancy; Derived by

```

automated computational analysis using gene prediction
 method: BestRefseq,BLAST. Supporting evidence includes
 similarity to: 1 mRNA
 /transcript_id="NM_003696.1"
 /db_xref="GI:4505520"
 /db_xref="LocusID:8590"
 CDS complement(1059885..1060868)
 /gene="OR6A1"
 /note="unclassified translation discrepancy"
 /codon_start=1
 /product="olfactory receptor, family 6, subfamily A,
 member 1"
 /protein_id="NP_003687.1"
 /db_xref="GI:4505521"
 /db_xref="LocusID:8590"
 gene 1110839..1111792
 /gene="LOC144124"
 /db_xref="InterimID:144124"
 mRNA 1110839..1111792
 /gene="LOC144124"
 /product="similar to Olfactory receptor 10A5 (HP3)
 (Olfactory receptor-like protein JCG6)"
 /note="Derived by automated computational analysis using
 gene prediction method: BLAST,GenomeScan. Supporting
 evidence includes similarity to: 1 mRNA"
 /transcript_id="XM_084745.1"
 /db_xref="GI:18605330"
 /db_xref="InterimID:144124"
 CDS 1110839..1111792
 /gene="LOC144124"
 /codon_start=1
 /protein_id="XP_084745.1"
 /db_xref="GI:18605331"
 /db_xref="InterimID:144124"
 gene 1128452..1135822
 /gene="LOC341276"
 /db_xref="InterimID:341276"
 mRNA join(1128452..1128507,1134847..1135822)
 /gene="LOC341276"
 /product="similar to hP4 olfactory receptor [Homo
 sapiens]"
 /note="Derived by automated computational analysis using
 gene prediction method: GenomeScan."
 /transcript_id="XM_291981.1"
 /db_xref="GI:29746586"
 /db_xref="InterimID:341276"
 CDS join(1128452..1128507,1134847..1135822)
 /gene="LOC341276"
 /codon_start=1
 /protein_id="XP_291981.1"
 /db_xref="GI:29746587"
 /db_xref="InterimID:341276"
 STS 1133437..1133561
 /gene="LOC341276"
 /standard_name="D11S3183"
 /db_xref="UniSTS:152429"
 gene 1141804..1142751
 /gene="LOC283297"
 /db_xref="InterimID:283297"
 mRNA 1141804..1142751

```

/ gene="LOC283297"
/ product="similar to Olfactory receptor 10A4 (HP2)
(Olfactory receptor-like protein JCG5)"
/ note="Derived by automated computational analysis using
gene prediction method: BLAST, GenomeScan. Supporting
evidence includes similarity to: 1 mRNA"
/ transcript_id="XM_208604.1"
/ db_xref="GI:27499430"
/ db_xref="InterimID:283297"
CDS
1141804..1142751
/ gene="LOC283297"
/ codon_start=1
/ protein_id="XP_208604.1"
/ db_xref="GI:27499431"
/ db_xref="InterimID:283297"
gene
complement(1156730..1157656)
/ gene="LOC120776"
/ db_xref="InterimID:120776"
mRNA
complement(1156730..1157656)
/ gene="LOC120776"
/ product="similar to Olfactory receptor 2D2 (Olfactory
receptor 11-610) (OR11-610) (HB2)"
/ note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/ transcript_id="XM_062286.2"
/ db_xref="GI:18605326"
/ db_xref="InterimID:120776"
CDS
complement(1156730..1157656)
/ gene="LOC120776"
/ codon_start=1
/ protein_id="XP_062286.2"
/ db_xref="GI:18605327"
/ db_xref="InterimID:120776"
gene
1186206..1187150
/ gene="LOC120775"
/ db_xref="InterimID:120775"
mRNA
1186206..1187150
/ gene="LOC120775"
/ product="similar to olfactory receptor MOR260-2 [Mus
musculus]"
/ note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/ transcript_id="XM_062285.1"
/ db_xref="GI:17461456"
/ db_xref="InterimID:120775"
CDS
1186206..1187150
/ gene="LOC120775"
/ codon_start=1
/ protein_id="XP_062285.1"
/ db_xref="GI:17461457"
/ db_xref="InterimID:120775"
gene
1191579..1253643
/ gene="ZNF215"
/ db_xref="LocusID:7762"
/ db_xref="MIM:605016"
mRNA
join(1191579..1191841,1192818..1192963,1197250..1197828,
1206727..1206809,1208239..1208371,1208702..1208797,
1220846..1222993)
/ gene="ZNF215"
/ product="zinc finger protein 215"

```



```

/note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 3 mRNAs"
/transcript_id="NM_013250.1"
/db_xref="GI:7019582"
/db_xref="LocusID:7762"
/db_xref="MIM:605016"
STS 1194876..1194999
/gene="ZNF215"
/standard_name="RH65576"
/db_xref="UniSTS:45472"
CDS join(1197429..1197828,1206727..1206809,1208239..1208371,
1208702..1208797,1220846..1221687)
/gene="ZNF215"
/note="unclassified translation discrepancy"
/codon_start=1
/product="zinc finger protein 215"
/protein_id="NP_037382.1"
/db_xref="GI:7019583"
/db_xref="LocusID:7762"
/db_xref="MIM:605016"
STS 1222751..1222937
/gene="ZNF215"
/standard_name="RH98892"
/db_xref="UniSTS:89130"
STS 1226896..1227009
/gene="ZNF215"
/standard_name="G17601"
/db_xref="UniSTS:42468"
misc_feature 1228270..1423366
/standard_name="RP11-715M10"
/note="FISH-mapped clone"
gene complement(1264474..1285503)
/gene="ZNF214"
/db_xref="LocusID:7761"
/db_xref="MIM:605015"
mRNA complement(join(1264474..1266711,1267865..1268011,
1285229..1285466))
/gene="ZNF214"
/product="zinc finger protein 214"
/note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 1 mRNA"
/transcript_id="NM_013249.1"
/db_xref="GI:7019580"
/db_xref="LocusID:7761"
/db_xref="MIM:605015"
CDS complement(join(1265018..1266711,1267865..1267991))
/gene="ZNF214"
/note="unclassified translation discrepancy"
/codon_start=1
/product="zinc finger protein 214"
/protein_id="NP_037381.1"
/db_xref="GI:7019581"
/db_xref="LocusID:7761"
/db_xref="MIM:605015"
STS 1279481..1279725
/standard_name="D11S1098"

```

```

gene      /db_xref="UniSTS:2653"
          1303743..1336464
          /gene="NALP14"
          /db_xref="LocusID:338323"
mRNA      join(1303743..1304031,1304870..1304941,1307544..1309140,
          1311824..1311988,1314827..1314994,1322833..1323003,
          1323436..1323606,1325050..1325220,1327489..1327659,
          1335442..1335612,1336329..1336464)
          /gene="NALP14"
          /product="NALP14"
          /note="Derived by automated computational analysis using
          gene prediction method: BLAST. Supporting evidence
          includes similarity to: 1 mRNA"
          /transcript_id="NM_176822.1"
          /db_xref="GI:28827812"
          /db_xref="LocusID:338323"
CDS       join(1303743..1304031,1304870..1304941,1307544..1309140,
          1311824..1311988,1314827..1314994,1322833..1323003,
          1323436..1323606,1325050..1325220,1327489..1327659,
          1335442..1335612,1336329..1336464)
          /gene="NALP14"
          /note="member of the NALP protein family involved in
          inflammation; contains NACHT, LRR and PYD domains"
          /codon_start=1
          /product="NALP14"
          /protein_id="NP_789792.1"
          /db_xref="GI:28827813"
          /db_xref="LocusID:338323"
gene      1354208..1355814
          /gene="HNRNPG-T"
          /db_xref="LocusID:27288"
          /db_xref="MIM:605444"
mRNA      1354208..1355814
          /gene="HNRNPG-T"
          /product="testes-specific heterogenous nuclear
          ribonucleoprotein G-T"
          /note="unclassified transcription discrepancy; Derived by
          automated computational analysis using gene prediction
          method: BestRefseq,BLAST. Supporting evidence includes
          similarity to: 3 mRNAs"
          /transcript_id="NM_014469.2"
          /db_xref="GI:8850216"
          /db_xref="LocusID:27288"
          /db_xref="MIM:605444"
CDS       1354277..1355455
          /gene="HNRNPG-T"
          /note="unclassified translation discrepancy"
          /codon_start=1
          /product="testes-specific heterogenous nuclear
          ribonucleoprotein G-T"
          /protein_id="NP_055284.2"
          /db_xref="GI:8850217"
          /db_xref="LocusID:27288"
          /db_xref="MIM:605444"
STS       1355315..1355478
          /gene="HNRNPG-T"
          /standard_name="RH104373"
          /db_xref="UniSTS:98698"
STS       1409450..1409762
          /standard_name="SHGC-84693"

```

```

STS      /db_xref="UniSTS:104092"
1421445..1421588
/standard_name="D11S2672"
STS      /db_xref="UniSTS:151898"
1463253..1463544
/standard_name="D11S3249"
STS      /db_xref="UniSTS:152494"
1484763..1485097
/standard_name="SHGC-142695"
gene     /db_xref="UniSTS:171597"
1503934..1735188
/gene="LOC143425"
mRNA     /db_xref="LocusID:143425"
join(1517343..1517487,1568195..1568546,1578551..1579097,
1681198..1681318,1683113..1683284,1685662..1685791)
/gene="LOC143425"
/product="similar to synaptotagmin V"
/note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 1 mRNA"
/transcript_id="NM_175733.1"
/db_xref="GI:28376626"
CDS      /db_xref="LocusID:143425"
join(1517343..1517487,1568195..1568546,1578551..1579097,
1681198..1681318,1683113..1683284,1685662..1685791)
/gene="LOC143425"
/note="unclassified translation discrepancy"
/codon_start=1
/product="similar to synaptotagmin V"
/protein_id="NP_783860.1"
/db_xref="GI:28376627"
STS      /db_xref="LocusID:143425"
1535937..1536135
/gene="LOC143425"
/standard_name="D11S1331"
misc_feature /db_xref="UniSTS:50340"
1535944..1536075
/gene="LOC143425"
/standard_name="RP11-205O15"
/note="FISH-mapped clone"
STS      1535944..1536075
/gene="LOC143425"
/standard_name="D11S1331"
/db_xref="UniSTS:30804"
STS      1544996..1545200
/gene="LOC143425"
/standard_name="G49572"
/db_xref="UniSTS:109241"
STS      1565296..1565624
/gene="LOC143425"
/standard_name="D11S3263"
/db_xref="UniSTS:152506"
STS      1580983..1581276
/gene="LOC143425"
/standard_name="SHGC-147933"
/db_xref="UniSTS:176105"
STS      1685400..1685512
/gene="LOC143425"
/standard_name="G49571"

```

```

STS      /db_xref="UniSTS:109240"
1731110..1731360
/gene="LOC143425"
/standard_name="G17607"
STS      /db_xref="UniSTS:66698"
1732056..1732199
/gene="LOC143425"
/standard_name="D11S690"
STS      /db_xref="UniSTS:148165"
1732595..1732750
/gene="LOC143425"
/standard_name="A006P43"
STS      /db_xref="UniSTS:56377"
1733936..1734063
/gene="LOC143425"
/standard_name="RH12015"
STS      /db_xref="UniSTS:23147"
1733968..1734112
/gene="LOC143425"
/standard_name="A005E31"
STS      /db_xref="UniSTS:52157"
1748648..1748941
/standard_name="SHGC-153704"
/db_xref="UniSTS:177894"
gene      1750698..1776061
/gene="LOC283298"
/db_xref="InterimID:283298"
mRNA      join(1750698..1751160,1753283..1753571,1774554..1776061)
/gene="LOC283298"
/product="similar to hypothetical protein 6720478C22 [Mus
musculus]"
/note="Derived by automated computational analysis using
gene prediction method: BLAST. Supporting evidence
includes similarity to: 1 mRNA"
/transcript_id="XM_208606.1"
/db_xref="GI:27499432"
/db_xref="InterimID:283298"
CDS      join(1751032..1751160,1753283..1753571,1774554..1775344)
/gene="LOC283298"
/codon_start=1
/protein_id="XP_208606.1"
/db_xref="GI:27499433"
/db_xref="InterimID:283298"
STS      1775780..1775967
/gene="LOC283298"
/standard_name="RH66484"
/db_xref="UniSTS:56766"
STS      1776058..1776343
/standard_name="G62644"
/db_xref="UniSTS:139624"
gene      1778942..1918921
/gene="PPFIBP2"
/db_xref="LocusID:8495"
/db_xref="MIM:603142"
mRNA      join(1778942..1779277,1814596..1814695,1830709..1830923,
1858288..1858380,1862716..1862829,1875447..1875578,
1886091..1886183,1890933..1891047,1893441..1893502,
1894615..1894690,1896081..1896184,1898023..1898090,
1899651..1899708,1900708..1900749,1904888..1905026,
1906635..1906776,1907454..1907582,1913543..1913693,

```

```

1913956..1914067,1914303..1914391,1914688..1914810,
1915996..1916121,1916812..1917000,1918180..1918914)
/gene="PPFIBP2"
/product="PTPRF interacting protein, binding protein 2
(liprin beta 2)"
/note="Derived by automated computational analysis using
gene prediction method: BLAST. Supporting evidence
includes similarity to: 5 mRNAs"
/transcript_id="XM_084578.6"
/db_xref="GI:27499434"
/db_xref="LocusID:8495"
/db_xref="MIM:603142"
CDS
join(1814632..1814695,1830709..1830923,1858288..1858380,
1862716..1862829,1875447..1875578,1886091..1886183,
1890933..1891047,1893441..1893502,1894615..1894690,
1896081..1896184,1898023..1898090,1899651..1899708,
1900708..1900749,1904888..1905026,1906635..1906776,
1907454..1907582,1913543..1913693,1913956..1914067,
1914303..1914391,1914688..1914810,1915996..1916121,
1916812..1917000,1918180..1918374)
/gene="PPFIBP2"
/codon_start=1
/protein_id="XP_084578.4"
/db_xref="GI:20561108"
/db_xref="LocusID:8495"
/db_xref="MIM:603142"
STS
1825408..1825712
/gene="PPFIBP2"
/standard_name="SHGC-82882"
/db_xref="UniSTS:104790"
STS
1825597..1825874
/gene="PPFIBP2"
/standard_name="SHGC-78819"
/db_xref="UniSTS:100821"
STS
1838829..1839104
/gene="PPFIBP2"
/standard_name="RH120212"
/db_xref="UniSTS:133205"
STS
1839513..1839733
/gene="PPFIBP2"
/standard_name="SHGC-112441"
/db_xref="UniSTS:182376"
STS
1852665..1852946
/gene="PPFIBP2"
/standard_name="SHGC-83011"
/db_xref="UniSTS:101281"
STS
1869059..1869256
/gene="PPFIBP2"
/standard_name="RH45476"
/db_xref="UniSTS:70768"
STS
1869144..1869412
/gene="PPFIBP2"
/standard_name="D11S1208"
/db_xref="UniSTS:10190"
STS
1887270..1887365
/gene="PPFIBP2"
/standard_name="SHGC-14320"
/db_xref="UniSTS:25229"
STS
1915876..1916177
/gene="PPFIBP2"

```

```

/standard_name="SHGC-154807"
/db_xref="UniSTS:178167"
STS 1916847..1916972
/gene="PPFIBP2"
/standard_name="G54152"
/db_xref="UniSTS:109389"
STS 1918662..1918896
/gene="PPFIBP2"
/standard_name="A004U29"
/db_xref="UniSTS:50995"
gene complement(1930261..1942376)
/gene="CYB5R2"
/db_xref="LocusID:51700"
mRNA complement(join(1930261..1930702,1931607..1931706,
1932884..1932969,1933634..1933717,1934361..1934490,
1934781..1934887,1937607..1937679,1937904..1938047,
1938575..1938657))
/gene="CYB5R2"
/product="cytochrome b5 reductase b5R.2"
/note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 1 mRNA"
/transcript_id="NM_016229.1"
/db_xref="GI:7706442"
/db_xref="LocusID:51700"
STS 1930270..1930470
/standard_name="STS-N90805"
/db_xref="UniSTS:79630"
CDS complement(join(1930532..1930702,1931607..1931706,
1932884..1932969,1933634..1933717,1934361..1934490,
1934781..1934887,1937607..1937679,1937904..1937981))
/gene="CYB5R2"
/note="unclassified translation discrepancy"
/codon_start=1
/product="cytochrome b5 reductase b5R.2"
/protein_id="NP_057313.1"
/db_xref="GI:7706443"
/db_xref="LocusID:51700"
STS 1932139..1932280
/standard_name="D11S4068"
/db_xref="UniSTS:154198"
STS 1932191..1932354
/standard_name="RH15972"
/db_xref="UniSTS:70824"
STS 1952358..1952598
/standard_name="D11S1996"
/db_xref="UniSTS:17642"
gene complement(1955111..1971866)
/gene="LOC341277"
/db_xref="InterimID:341277"
mRNA complement(join(1955111..1955169,1956425..1956556,
1957058..1957139,1960214..1960344,1960726..1960808,
1961774..1962061,1962181..1962271,1964222..1964245,
1965768..1965957,1966796..1966947,1967188..1967283,
1967629..1967801,1969170..1969261,1970037..1970146,
1971779..1971866))
/gene="LOC341277"
/product="similar to hypothetical protein 9230106D23 [Mus
musculus]"

```

```

/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_291982.1"
/db_xref="GI:29746588"
/db_xref="InterimID:341277"
CDS complement(join(1955111..1955169,1956425..1956556,
1957058..1957139,1960214..1960344,1960726..1960808,
1961774..1962061,1962181..1962271,1964222..1964245,
1965768..1965957,1966796..1966947,1967188..1967283,
1967629..1967801,1969170..1969261,1970037..1970146,
1971779..1971866))
/gene="LOC341277"
/codon_start=1
/protein_id="XP_291982.1"
/db_xref="GI:29746589"
/db_xref="InterimID:341277"
misc_feature 1974740..2100479
/standard_name="RP11-25D22"
/note="FISH-mapped clone"
misc_feature 1982544..2156690
/standard_name="RP11-399N15"
/note="FISH-mapped clone"
gene 1993995..1994855
/gene="LOC120061"
/db_xref="InterimID:120061"
mRNA 1993995..1994855
/gene="LOC120061"
/product="similar to seven transmembrane helix receptor
[Homo sapiens]"
/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_061838.2"
/db_xref="GI:22061586"
/db_xref="InterimID:120061"
CDS 1993995..1994855
/gene="LOC120061"
/codon_start=1
/protein_id="XP_061838.2"
/db_xref="GI:22061587"
/db_xref="InterimID:120061"
gene 2011452..2012374
/gene="LOC120062"
/db_xref="InterimID:120062"
mRNA join(2011452..2011768,2011783..2012374)
/gene="LOC120062"
/product="similar to olfactory receptor MOR204-2 [Mus
musculus]"
/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_061839.2"
/db_xref="GI:22061590"
/db_xref="InterimID:120062"
CDS join(2011452..2011768,2011783..2012374)
/gene="LOC120062"
/codon_start=1
/protein_id="XP_061839.2"
/db_xref="GI:22061591"
/db_xref="InterimID:120062"
STS 2018101..2018226
/standard_name="D11S3672"

```

```

gene      /db_xref="UniSTS:152906"
          complement(2038353..2039277)
          /gene="LOC341278"
mRNA      /db_xref="InterimID:341278"
          complement(join(2038353..2038972,2039061..2039277))
          /gene="LOC341278"
          /product="similar to olfactory receptor MOR204-11 [Mus
musculus]"
          /note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
          /transcript_id="XM_291983.1"
          /db_xref="GI:29746590"
          /db_xref="InterimID:341278"
CDS       complement(join(2038353..2038972,2039061..2039277))
          /gene="LOC341278"
          /codon_start=1
          /protein_id="XP_291983.1"
          /db_xref="GI:29746591"
          /db_xref="InterimID:341278"
gene      2049160..2049870
          /gene="LOC120064"
          /db_xref="InterimID:120064"
mRNA      join(2049160..2049218,2049261..2049457,2049567..2049687,
2049738..2049870)
          /gene="LOC120064"
          /product="similar to 60S ribosomal protein L7A (Surfeit
locus protein 3)"
          /note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
          /transcript_id="XM_061841.1"
          /db_xref="GI:17472928"
          /db_xref="InterimID:120064"
CDS       join(2049160..2049218,2049261..2049457,2049567..2049687,
2049738..2049870)
          /gene="LOC120064"
          /codon_start=1
          /protein_id="XP_061841.1"
          /db_xref="GI:17472929"
          /db_xref="InterimID:120064"
gene      complement(2061437..2062405)
          /gene="JCG3"
          /db_xref="LocusID:120065"
mRNA      complement(2061437..2062405)
          /gene="JCG3"
          /product="olfactory receptor-like protein JCG3"
          /note="Derived by automated computational analysis using
gene prediction method: BestRefseq,BLAST. Supporting
evidence includes similarity to: 3 mRNAs"
          /transcript_id="NM_153444.1"
          /db_xref="GI:23592221"
          /db_xref="LocusID:120065"
CDS       complement(2061437..2062405)
          /gene="JCG3"
          /codon_start=1
          /product="olfactory receptor-like protein JCG3"
          /protein_id="NP_703145.1"
          /db_xref="GI:23592222"
          /db_xref="LocusID:120065"
gene      complement(2090500..2091435)
          /gene="JCG1"

```


mRNA
 /db_xref="LocusID:120066"
 complement(2090500..2091435)
 /gene="JCG1"
 /product="olfactory receptor-like protein JCG1"
 /note="Derived by automated computational analysis using
 gene prediction method: BestRefseq, BLAST. Supporting
 evidence includes similarity to: 2 mRNAs"
 /transcript_id="NM_153445.1"
 /db_xref="GI:23592229"
 /db_xref="LocusID:120066"
 CDS
 complement(2090500..2091435)
 /gene="JCG1"
 /codon_start=1
 /product="olfactory receptor-like protein JCG1"
 /protein_id="NP_703146.1"
 /db_xref="GI:23592230"
 /db_xref="LocusID:120066"
 STS
 2092558..2092877
 /standard_name="SHGC-149151"
 /db_xref="UniSTS:176832"
 misc_feature
 2100330..2100479
 /standard_name="RP11-799H15"
 /note="FISH-mapped clone"
 STS
 2100330..2100479
 /standard_name="SHGC-30914"
 /db_xref="UniSTS:34295"
 gene
 2114514..2115098
 /gene="OR5E1P"
 /pseudo
 /db_xref="LocusID:26343"
 gene
 complement(2116214..2171418)
 /gene="LOC283299"
 /db_xref="InterimID:283299"
 mRNA
 complement(join(2116214..2117787,2120346..2120426,
 2144470..2144546,2145058..2145222,2146552..2146612,
 2147419..2147536,2148323..2148396,2171066..2171418))
 /gene="LOC283299"
 /product="LOC283299"
 /note="Derived by automated computational analysis using
 gene prediction method: BLAST. Supporting evidence
 includes similarity to: 1 mRNA"
 /transcript_id="XM_210965.1"
 /db_xref="GI:27499435"
 /db_xref="InterimID:283299"
 CDS
 complement(2116906..2117328)
 /gene="LOC283299"
 /codon_start=1
 /protein_id="XP_210965.1"
 /db_xref="GI:27499436"
 /db_xref="InterimID:283299"
 misc_feature
 2145539..2281898
 /standard_name="RP11-21N2"
 /note="FISH-mapped clone"
 gene
 complement(2193181..2194125)
 /gene="LOC341279"
 /db_xref="InterimID:341279"
 mRNA
 complement(2193181..2194125)
 /gene="LOC341279"
 /product="similar to seven transmembrane helix receptor
 [Homo sapiens]"

```

/Note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_291985.1"
/db_xref="GI:29746592"
/db_xref="InterimID:341279"
complement(2193181..2194125)
/gene="LOC341279"
/codon_start=1
/protein_id="XP_291985.1"
/db_xref="GI:29746593"
/db_xref="InterimID:341279"
complement(2204039..2204983)
/gene="OR10A3"
/db_xref="LocusID:26496"
complement(2204039..2204983)
/gene="OR10A3"
/product="olfactory receptor, family 10, subfamily A,
member 3"
/Note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_291986.1"
/db_xref="GI:29746594"
/db_xref="LocusID:26496"
complement(2204039..2204983)
/gene="OR10A3"
/codon_start=1
/protein_id="XP_291986.1"
/db_xref="GI:29746595"
/db_xref="LocusID:26496"
2213429..2213723
/standard_name="SHGC-142522"
/db_xref="UniSTS:171506"
complement(2225107..2228958)
/gene="NALP10"
/db_xref="LocusID:338322"
complement(join(2225107..2226785,2228670..2228958))
/gene="NALP10"
/product="NALP10"
/Note="Derived by automated computational analysis using
gene prediction method: BLAST. Supporting evidence
includes similarity to: 1 mRNA"
/transcript_id="NM_176821.1"
/db_xref="GI:28827806"
/db_xref="LocusID:338322"
complement(join(2225107..2226785,2228670..2228958))
/gene="NALP10"
/Note="member of the NALP protein family involved in
inflammation; contains NACHT and PYD domains; NALPs"
/codon_start=1
/product="NALP10"
/protein_id="NP_789791.1"
/db_xref="GI:28827807"
/db_xref="LocusID:338322"
2235714..2263623
/gene="EIF3S5"
/db_xref="LocusID:8665"
/db_xref="MIM:603914"
2236942..2237202
/gene="EIF3S5"
/standard_name="D11S2839"

```

```

mRNA      /db_xref="UniSTS:152025"
          join(2252810..2253179,2257244..2257314,2257547..2257626,
          2258350..2258487,2259889..2259980,2260445..2260581,
          2260717..2260830,2261408..2261627)
          /gene="EIF3S5"
          /product="eukaryotic translation initiation factor 3,
          subunit 5 epsilon, 47kDa"
          /note="unclassified transcription discrepancy; Derived by
          automated computational analysis using gene prediction
          method: BestRefseq,BLAST. Supporting evidence includes
          similarity to: 1 mRNA"
          /transcript_id="NM_003754.1"
          /db_xref="GI:4503518"
          /db_xref="LocusID:8665"
          /db_xref="MIM:603914"
CDS        join(2252816..2253179,2257244..2257314,2257547..2257626,
          2258350..2258487,2259889..2259980,2260445..2260581,
          2260717..2260830,2261408..2261485)
          /gene="EIF3S5"
          /note="eukaryotic translation initiation factor 3, subunit
          5 (epsilon, 47kD)"
          /codon_start=1
          /product="eukaryotic translation initiation factor 3,
          subunit 5 epsilon, 47kDa"
          /protein_id="NP_003745.1"
          /db_xref="GI:4503519"
          /db_xref="LocusID:8665"
          /db_xref="MIM:603914"
STS        2259514..2259666
          /gene="EIF3S5"
          /standard_name="D11S1152"
          /db_xref="UniSTS:19122"
STS        2265903..2266014
          /standard_name="RH18331"
          /db_xref="UniSTS:81654"
STS        2267138..2267225
          /standard_name="STS-F03421"
          /db_xref="UniSTS:55985"
STS        2281505..2281813
          /standard_name="SHGC-78923"
          /db_xref="UniSTS:182491"
gene       2284729..2368411
          /gene="TUB"
          /db_xref="LocusID:7275"
          /db_xref="MIM:601197"
mRNA       join(2304096..2304491,2305108..2305155,2355073..2355124,
          2355532..2355694,2359509..2359652,2360961..2361128,
          2362148..2362269,2362691..2362888,2363177..2363289,
          2364221..2364338,2365966..2366064,2366289..2366460,
          2366949..2368411)
          /gene="TUB"
          /product="tubby homolog (mouse)"
          /note="unclassified transcription discrepancy; Derived by
          automated computational analysis using gene prediction
          method: BestRefseq,BLAST. Supporting evidence includes
          similarity to: 2 mRNAs"
          /transcript_id="NM_003320.2"
          /db_xref="GI:19923166"
          /db_xref="LocusID:7275"
          /db_xref="MIM:601197"

```

CDS join(2304337..2304491,2305108..2305155,2355073..2355124,
 2355532..2355694,2359509..2359652,2360961..2361128,
 2362148..2362269,2362691..2362888,2363177..2363289,
 2364221..2364338,2365966..2366064,2366289..2366460,
 2366949..2367082)
 /gene="TUB"
 /function="unknown"
 /note="tubby (mouse) homolog"
 /codon_start=1
 /product="tubby homolog (mouse)"
 /protein_id="NP_003311.2"
 /db_xref="GI:19923167"
 /db_xref="LocusID:7275"
 /db_xref="MIM:601197"
 STS 2358483..2358682
 /gene="TUB"
 /standard_name="RH36564"
 /db_xref="UniSTS:55145"
 gene complement(2371564..2434486)
 /gene="FLJ11608"
 /db_xref="LocusID:79608"
 mRNA complement(join(2374412..2376600,2392120..2392265,
 2402839..2402932,2403733..2403808,2405428..2405654,
 2434327..2434483))
 /gene="FLJ11608"
 /product="hypothetical protein FLJ11608"
 /note="unclassified transcription discrepancy; Derived by
 automated computational analysis using gene prediction
 method: BestRefseq,BLAST. Supporting evidence includes
 similarity to: 1 mRNA"
 /transcript_id="NM_024557.2"
 /db_xref="GI:21362039"
 /db_xref="LocusID:79608"
 STS 2374425..2374555
 /standard_name="WI-14382"
 /db_xref="UniSTS:24731"
 CDS complement(join(2376161..2376600,2392120..2392265,
 2402839..2402932,2403733..2403808,2405428..2405654,
 2434327..2434450))
 /gene="FLJ11608"
 /note="unclassified translation discrepancy"
 /codon_start=1
 /evidence=not_experimental
 /product="hypothetical protein FLJ11608"
 /protein_id="NP_078833.2"
 /db_xref="GI:21362040"
 /db_xref="LocusID:79608"
 STS 2463789..2464120
 /standard_name="SHGC-148637"
 /db_xref="UniSTS:176517"
 STS 2478374..2478714
 /standard_name="D11S3436"
 /db_xref="UniSTS:152677"
 gene complement(2489771..2534177)
 /gene="LM01"
 /db_xref="LocusID:4004"
 /db_xref="MIM:186921"
 mRNA complement(join(2489771..2490182,2492436..2492561,
 2495752..2495965,2528799..2529320))
 /gene="LM01"

```

/product="LIM domain only 1 (rhombotin 1)"
/note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method:~BestRefseq,BLAST. Supporting evidence includes
similarity to: 3 mRNAs"
/transcript_id="NM_002315.1"
/db_xref="GI:4505004"
/db_xref="LocusID:4004"
/db_xref="MIM:186921"
STS      2489794..2489968
          /standard_name="D11S4594"
          /db_xref="UniSTS:29757"
STS      2489856..2490012
          /standard_name="LMO1"
          /db_xref="UniSTS:26133"
CDS      complement(join(2490077..2490182,2492436..2492561,
2495752..2495965,2528799..2528823))
          /gene="LMO1"
          /note="Lmol"
          /codon_start=1
          /product="LIM domain only 1"
          /protein_id="NP_002306.1"
          /db_xref="GI:4505005"
          /db_xref="LocusID:4004"
          /db_xref="MIM:186921"
STS      2578643..2578975
          /standard_name="SHGC-148827"
          /db_xref="UniSTS:176632"
STS      2597737..2597892
          /standard_name="G29013"
          /db_xref="UniSTS:10871"
STS      2613526..2613799
          /standard_name="D11S3261"
          /db_xref="UniSTS:152504"
misc_feature 2634677..2634828
          /standard_name="CTB-2P10"
          /note="FISH-mapped clone"
STS      2634677..2634828
          /standard_name="D11S932"
          /db_xref="UniSTS:67475"
STS      2636239..2636339
          /standard_name="D11S2704"
          /db_xref="UniSTS:151927"
STS      2652365..2652662
          /standard_name="SHGC-145524"
          /db_xref="UniSTS:174627"
gene      complement(2657332..2798958)
          /gene="STK33"
          /db_xref="LocusID:65975"
STS      2657354..2657528
          /standard_name="SGC44503"
          /db_xref="UniSTS:79706"
mRNA      complement(join(2657371..2658171,2678956..2679153,
2700955..2701040,2701488..2701600,2706139..2706214,
2718283..2718367,2720205..2720293,2722802..2722940,
2727266..2727370,2730170..2730283,2738624..2738737,
2740142..2741285))
          /gene="STK33"
          /product="serine/threonine kinase 33"
          /note="unclassified transcription discrepancy; Derived by

```

```

automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 1 mRNA"
/transcript_id="NM_030906.1"
/db_xref="GI:23943881"
/db_xref="LocusID:65975"
STS      2657383..2657494
         /standard_name="SHGC-44503"
         /db_xref="UniSTS:25962"
STS      2657665..2657786
         /standard_name="RH92437"
         /db_xref="UniSTS:90136"
CDS      complement(join(2657971..2658171,2678956..2679153,
2700955..2701040,2701488..2701600,2706139..2706214,
2718283..2718367,2720205..2720293,2722802..2722940,
2727266..2727370,2730170..2730283,2738624..2738737,
2740142..2740366))
         /gene="STK33"
         /codon_start=1
         /product="serine/threonine kinase 33"
         /protein_id="NP_112168.1"
         /db_xref="GI:23943882"
         /db_xref="LocusID:65975"
STS      2742574..2742720
         /standard_name="D11S431"
         /db_xref="UniSTS:148537"
STS      2762937..2763250
         /standard_name="D11S3426"
         /db_xref="UniSTS:152667"
CONTIG   join(complement(AC131574.4:2930..166214),AC025016.8:1..74840,
complement(AC111177.15:1..165682),AC022762.8:54839..186604,
AC068733.12:8771..191656,AC084337.7:42081..112295,
AC009796.6:67320..192239,AC091564.12:45902..211735,
AC087280.11:44766..173611,AC090160.6:30193..170008,
complement(AC100875.3:1..75276),AC027804.7:42630..172272,
AC060799.6:15779..152164,complement(AC107884.15:1348..164472),
complement(AC104237.2:1..164732),AC021427.10:34710..174147,
AC044810.7:112096..194297,complement(AC124259.6:1..43031),
AC116456.12:43903..146502,complement(AC129895.5:55633..103080),
complement(AC091013.7:4558..223741),AC105357.7:1..167772)
//

```

Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

May 2 2003 16:47:12



PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Bio

Search for

Limits

Preview/Index

History

Clipboard

Details

Show:

1: NT_009334[gi:15314816] This record was removed as a result of standard genome annotation processing. See the genome build documentation at <http://www.ncbi.nlm.nih.gov/genome/guide/build.html> for further information, or contact info@ncbi.nlm.nih.gov.

LOCUS NT_009334 5196829 bp DNA linear CON 27-AUG-2001
 DEFINITION Homo sapiens chromosome 11 working draft sequence segment.
 ACCESSION NT_009334
 VERSION NT_009334.5 GI:15314816
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 5196829)
 AUTHORS NCBI Annotation Project.
 TITLE Direct Submission
 JOURNAL Submitted (23-AUG-2001) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA
 COMMENT GENOME ANNOTATION REFSEQ: NCBI contigs are derived from assembled
 genomic sequence data.
 Also see:
 Documentation of NCBI's Annotation Process

On Aug 27, 2001 this sequence version replaced gi:14774332.
 COMPLETENESS: not full length.

FEATURES Location/Qualifiers
 source 1..5196829
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="11"
 gene complement(637..23170)
 /gene="IGSF4"
 /note="synonyms: ST17, TSLC1"
 /db_xref="LocusID:23705"
 /db_xref="MIM:605686"
 mRNA complement(join(637..738,11866..12022,14104..14241,
 21248..21400,23022..23170))
 /gene="IGSF4"
 /product="immunoglobulin superfamily, member 4"
 /note="Derived by automated computational analysis.
 Supporting evidence includes similarity to: 1 mRNA"
 /transcript_id="XM_011956.2"
 /db_xref="GI:13641511"
 /db_xref="LocusID:23705"
 /db_xref="MIM:605686"
 CDS complement(join(711..738,11866..12022,14104..14224))
 /gene="IGSF4"

/codon_start=1
/protein_id="XP_011956.2"
/db_xref="GI:13641512"
/db_xref="LocusID:23705"
/db_xref="MIM:605686"
variation 5023
/allele="T"
/allele="G"
/db_xref="dbSNP:1938736"
STS 18955..19104
/standard_name="SHGC-13348"
/note="WARNING: map location ambiguous"
/db_xref="UniSTS:10329"
variation 19821
/allele="T"
/allele="C"
/db_xref="dbSNP:2002897"
variation 20012
/allele="T"
/allele="G"
/db_xref="dbSNP:947802"
variation 23838
/allele="T"
/allele="C"
/db_xref="dbSNP:2186421"
variation 26986
/allele="T"
/allele="C"
/db_xref="dbSNP:2186420"
variation 34654
/allele="C"
/allele="A"
/db_xref="dbSNP:1892773"
STS 39988..40154
/standard_name="C95588"
/db_xref="UniSTS:17132"
variation 47567
/allele="G"
/allele="C"
/db_xref="dbSNP:2154690"
variation 70997
/allele="C"
/allele="G"
/db_xref="dbSNP:881210"
variation 71123
/allele="C"
/allele="T"
/db_xref="dbSNP:881211"
variation 71693
/allele="G"
/allele="C"
/db_xref="dbSNP:2014270"
variation 72568
/allele="C"
/allele="A"
/db_xref="dbSNP:1234501"
variation 72607
/allele="T"
/allele="C"
/db_xref="dbSNP:1234500"

variation 72636
/allele="G"
/allele="C"
/db_xref="dbSNP:1234499"
variation 73107
/allele="G"
/allele="C"
/db_xref="dbSNP:1234498"
STS 75120..75385
/standard_name="C95642"
/db_xref="UniSTS:72630"
variation 78746
/allele="T"
/allele="C"
/db_xref="dbSNP:2187988"
variation 87464
/allele="T"
/allele="G"
/db_xref="dbSNP:1024317"
variation 90977
/allele="G"
/allele="A"
/db_xref="dbSNP:2040456"
variation 91321
/allele="G"
/allele="C"
/db_xref="dbSNP:2040455"
variation 91355
/allele="G"
/allele="A"
/db_xref="dbSNP:2157613"
variation 91357
/allele="G"
/allele="A"
/db_xref="dbSNP:2105977"
variation 91374
/allele="G"
/allele="A"
/db_xref="dbSNP:2040454"
variation 91531
/allele="C"
/allele="A"
/db_xref="dbSNP:2157612"
variation 94908
/allele="T"
/allele="C"
/db_xref="dbSNP:970196"
variation 101688
/allele="T"
/allele="C"
/db_xref="dbSNP:988873"
STS 114655..114782
/standard_name="C95583"
/db_xref="UniSTS:56066"
variation 122960
/allele="G"
/allele="A"
/db_xref="dbSNP:2105976"
variation 123170
/allele="A"

```

/allele="G"
/db_xref="dbSNP:715295"
variation 127118
/allele="G"
/allele="C"
/db_xref="dbSNP:2027898"
variation 132714
/allele="T"
/allele="G"
/db_xref="dbSNP:1013416"
variation 133333
/allele="G"
/allele="A"
/db_xref="dbSNP:1986100"
variation 136264
/allele="G"
/allele="A"
/db_xref="dbSNP:2105982"
variation 141345
/allele="C"
/allele="A"
/db_xref="dbSNP:2097577"
variation 141394
/allele="G"
/allele="C"
/db_xref="dbSNP:2040137"
variation 141395
/allele="T"
/allele="A"
/db_xref="dbSNP:2040136"
variation 141852
/allele="T"
/allele="G"
/db_xref="dbSNP:2157614"
variation 147266
/allele="T"
/allele="C"
/db_xref="dbSNP:1013583"
variation 147557
/allele="T"
/allele="A"
/db_xref="dbSNP:1013582"
variation 147599
/allele="T"
/allele="C"
/db_xref="dbSNP:1013581"
variation 150029
/allele="T"
/allele="C"
/db_xref="dbSNP:2105981"
variation 154058
/allele="T"
/allele="C"
/db_xref="dbSNP:2027617"
variation 154086
/allele="T"
/allele="C"
/db_xref="dbSNP:2027616"
gene complement(154988..156160)
/gene="PRO1966"

```

mRNA /db_xref="LocusID:55475"
complement(154988..156160)
/gene="PRO1966"
/product="hypothetical protein PRO1966"
/note="Derived by automated computational analysis.
Supporting evidence includes similarity to: 1 mRNA"
/transcript_id="XM_052145.1"
/db_xref="GI:14774322"
/db_xref="LocusID:55475"

CDS complement(155593..155751)
/gene="PRO1966"
/codon_start=1
/protein_id="XP_052145.1"
/db_xref="GI:14774323"
/db_xref="LocusID:55475"

variation 156489
/allele="G"
/allele="A"
/db_xref="dbSNP:2027615"

variation 156594
/allele="T"
/allele="C"
/db_xref="dbSNP:2105980"

variation 156596
/allele="T"
/allele="C"
/db_xref="dbSNP:2105979"

variation 156787
/allele="G"
/allele="A"
/db_xref="dbSNP:2105978"

variation 156843
/allele="G"
/allele="A"
/db_xref="dbSNP:1632809"

variation 156846
/allele="G"
/allele="A"
/db_xref="dbSNP:1632808"

variation 156933
/allele="G"
/allele="A"
/db_xref="dbSNP:1632807"

variation 156984
/allele="G"
/allele="A"
/db_xref="dbSNP:1632806"

variation 157100
/allele="G"
/allele="C"
/db_xref="dbSNP:1783282"

variation 157852
/allele="C"
/allele="A"
/db_xref="dbSNP:220851"

variation 158023
/allele="T"
/allele="C"
/db_xref="dbSNP:1398261"

variation 158267

variation /allele="T"
/allele="A"
/db_xref="dbSNP:1398260"
160815
/allele="T"
/allele="C"
/db_xref="dbSNP:220850"
variation 161418
/allele="T"
/allele="A"
/db_xref="dbSNP:220849"
variation 162895
/allele="T"
/allele="G"
/db_xref="dbSNP:220848"
variation 165546
/allele="T"
/allele="G"
/db_xref="dbSNP:183394"
variation 166184
/allele="C"
/allele="T"
/db_xref="dbSNP:220867"
variation 168988
/allele="C"
/allele="A"
/db_xref="dbSNP:2213890"
variation 170493
/allele="A"
/allele="T"
/db_xref="dbSNP:170224"
STS 172853..173125
/standard_name="C95631"
/db_xref="UniSTS:4464"
variation 173237
/allele="C"
/allele="T"
/db_xref="dbSNP:220868"
variation 174496
/allele="T"
/allele="C"
/db_xref="dbSNP:220869"
variation 174828
/allele="A"
/allele="C"
/db_xref="dbSNP:1398257"
variation 177645
/allele="C"
/allele="T"
/db_xref="dbSNP:220870"
variation 177739
/allele="G"
/allele="A"
/db_xref="dbSNP:220871"
variation 178039
/allele="C"
/allele="A"
/db_xref="dbSNP:2027900"
variation 178044
/allele="C"

variation /allele="A"
/db_xref="dbSNP:2027899"
178825
/allele="A"
/allele="G"
variation /db_xref="dbSNP:220872"
179042
/allele="A"
/allele="G"
variation /db_xref="dbSNP:220873"
179404
/allele="C"
/allele="T"
variation /db_xref="dbSNP:220874"
180442
/allele="A"
/allele="G"
variation /db_xref="dbSNP:220875"
180581
/allele="A"
/allele="G"
variation /db_xref="dbSNP:183395"
180934
/allele="G"
/allele="A"
variation /db_xref="dbSNP:220876"
180995
/allele="C"
/allele="T"
variation /db_xref="dbSNP:183396"
182979
/allele="C"
/allele="G"
variation /db_xref="dbSNP:220877"
183819
/allele="G"
/allele="A"
variation /db_xref="dbSNP:220832"
184047
/allele="T"
/allele="A"
variation /db_xref="dbSNP:220831"
184777
/allele="T"
/allele="C"
variation /db_xref="dbSNP:220830"
188012
/allele="T"
/allele="C"
variation /db_xref="dbSNP:170221"
188749
/allele="C"
/allele="A"
variation /db_xref="dbSNP:220829"
189265
/allele="T"
/allele="C"
variation /db_xref="dbSNP:220828"
192953
/allele="C"

```

/allele="T"
/db_xref="dbSNP:1398259"
variation 193644
/allele="G"
/allele="T"
/db_xref="dbSNP:220841"
variation 194632
/allele="A"
/allele="T"
/db_xref="dbSNP:220842"
variation 195995
/allele="T"
/allele="C"
/db_xref="dbSNP:220843"
variation 197729
/allele="T"
/allele="C"
/db_xref="dbSNP:220844"
variation 197836
/allele="G"
/allele="A"
/db_xref="dbSNP:220845"
variation 198092
/allele="G"
/allele="A"
/db_xref="dbSNP:220846"
variation 198577
/allele="T"
/allele="C"
/db_xref="dbSNP:220847"
STS 199807..199951
/standard_name="D11S908"
/db_xref="UniSTS:146591"
STS 199823..199948
/standard_name="AFM120xe9"
/db_xref="UniSTS:65834"
STS 204668..204936
/standard_name="C95632"
/db_xref="UniSTS:11152"
variation 206524
/allele="A"
/allele="C"
/db_xref="dbSNP:220860"
variation 206652
/allele="G"
/allele="T"
/db_xref="dbSNP:220861"
variation 207764
/allele="G"
/allele="T"
/db_xref="dbSNP:1961719"
variation 208379
/allele="C"
/allele="T"
/db_xref="dbSNP:220862"
variation 208635
/allele="G"
/allele="A"
/db_xref="dbSNP:220863"
variation 209091

```

	/allele="T"
	/allele="C"
variation	/db_xref="dbSNP:220864"
	209410
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:220865"
	210543
	/allele="C"
	/allele="A"
variation	/db_xref="dbSNP:220866"
	210997
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:2102593"
	212569
	/allele="C"
	/allele="A"
variation	/db_xref="dbSNP:220833"
	212612
	/allele="T"
	/allele="C"
variation	/db_xref="dbSNP:170222"
	212647
	/allele="T"
	/allele="G"
variation	/db_xref="dbSNP:220834"
	212716
	/allele="C"
	/allele="A"
variation	/db_xref="dbSNP:178326"
	212725
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:220835"
	214088
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:2027618"
	214331
	/allele="T"
	/allele="C"
variation	/db_xref="dbSNP:220836"
	217644
	/allele="T"
	/allele="C"
STS	/db_xref="dbSNP:1632804"
	218465..218634
	/standard_name="C95578"
	/db_xref="UniSTS:10575"
variation	219746
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:220852"
	220517
	/allele="C"
	/allele="A"
variation	/db_xref="dbSNP:220853"
	220545
	/allele="G"

variation /allele="A"
/db_xref="dbSNP:220854"
221763
/allele="C"
/allele="T"
/db_xref="dbSNP:220855"
variation 222927
/allele="C"
/allele="T"
/db_xref="dbSNP:220856"
variation 222935
/allele="C"
/allele="T"
/db_xref="dbSNP:220857"
variation 223907
/allele="G"
/allele="C"
/db_xref="dbSNP:220858"
variation 224033
/allele="T"
/allele="C"
/db_xref="dbSNP:170223"
variation 224531
/allele="T"
/allele="C"
/db_xref="dbSNP:220859"
variation 226494
/allele="G"
/allele="A"
/db_xref="dbSNP:220837"
variation 226562
/allele="A"
/allele="G"
/db_xref="dbSNP:220838"
variation 228857
/allele="T"
/allele="A"
/db_xref="dbSNP:183393"
variation 231051
/allele="C"
/allele="A"
/db_xref="dbSNP:160604"
STS 231171..231442
/standard_name="SHGC-104384"
/db_xref="UniSTS:135631"
variation 231556
/allele="C"
/allele="A"
/db_xref="dbSNP:220839"
variation 232928
/allele="T"
/allele="A"
/db_xref="dbSNP:314473"
variation 232941
/allele="C"
/allele="G"
/db_xref="dbSNP:544083"
variation 232943
/allele="A"
/allele="G"

variation	/db_xref="dbSNP:544086" 233423 /allele="G" /allele="A"
variation	/db_xref="dbSNP:220840" 233593 /allele="T" /allele="C"
STS	/db_xref="dbSNP:314474" 233631..233837 /standard_name="C95582"
variation	/db_xref="UniSTS:67149" 234223 /allele="T" /allele="C"
variation	/db_xref="dbSNP:314475" 234765 /allele="T" /allele="C"
variation	/db_xref="dbSNP:314476" 235961 /allele="T" /allele="C"
variation	/db_xref="dbSNP:1979326" 236546 /allele="C" /allele="A"
variation	/db_xref="dbSNP:221315" 237717 /allele="A" /allele="G"
variation	/db_xref="dbSNP:1155756" 237854 /allele="C" /allele="T"
variation	/db_xref="dbSNP:314486" 239782 /allele="G" /allele="A"
variation	/db_xref="dbSNP:314487" 241999 /allele="A" /allele="T"
variation	/db_xref="dbSNP:314488" 244316 /allele="T" /allele="A"
variation	/db_xref="dbSNP:314489" 244595 /allele="A" /allele="G"
variation	/db_xref="dbSNP:724737" 246364 /allele="G" /allele="A"
variation	/db_xref="dbSNP:314490" 247668 /allele="G" /allele="C"
	/db_xref="dbSNP:314491"

variation 247901
/allele="T"
/allele="C"
/db_xref="dbSNP:314492"

variation 248915
/allele="T"
/allele="A"
/db_xref="dbSNP:314493"

variation 249059
/allele="T"
/allele="C"
/db_xref="dbSNP:314494"

variation 249830
/allele="T"
/allele="G"
/db_xref="dbSNP:314495"

variation 250034
/allele="T"
/allele="A"
/db_xref="dbSNP:314496"

variation 254389
/allele="T"
/allele="G"
/db_xref="dbSNP:314497"

variation 254905
/allele="T"
/allele="C"
/db_xref="dbSNP:314498"

variation 255187
/allele="C"
/allele="A"
/db_xref="dbSNP:314499"

variation 255632
/allele="T"
/allele="G"
/db_xref="dbSNP:314500"

variation 256645
/allele="G"
/allele="C"
/db_xref="dbSNP:314501"

variation 257713
/allele="T"
/allele="C"
/db_xref="dbSNP:314502"

variation 259224
/allele="T"
/allele="G"
/db_xref="dbSNP:1460909"

variation 259225
/allele="T"
/allele="C"
/db_xref="dbSNP:1460908"

variation 259318
/allele="T"
/allele="C"
/db_xref="dbSNP:314503"

variation 259904
/allele="T"
/allele="C"
/db_xref="dbSNP:314504"

variation 260968
/allele="G"
/allele="A"
/db_xref="dbSNP:314505"

variation 261314
/allele="C"
/allele="T"
/db_xref="dbSNP:314506"

variation 261707
/allele="T"
/allele="G"
/db_xref="dbSNP:314507"

variation 262065
/allele="G"
/allele="A"
/db_xref="dbSNP:314508"

variation 262447
/allele="T"
/allele="C"
/db_xref="dbSNP:314509"

STS 263090..263397
/standard_name="SHGC-154812"
/db_xref="UniSTS:178169"

variation 263163
/allele="G"
/allele="A"
/db_xref="dbSNP:1531369"

variation 264383
/allele="T"
/allele="C"
/db_xref="dbSNP:314510"

variation 264825
/allele="T"
/allele="C"
/db_xref="dbSNP:314511"

variation 265351
/allele="T"
/allele="C"
/db_xref="dbSNP:314512"

variation 265755
/allele="G"
/allele="A"
/db_xref="dbSNP:314513"

STS 268503..268613
/standard_name="C95603"
/db_xref="UniSTS:39332"

variation 269145
/allele="T"
/allele="C"
/db_xref="dbSNP:314514"

variation 269829
/allele="C"
/allele="A"
/db_xref="dbSNP:314515"

STS 270812..271162
/standard_name="D11S3323"
/db_xref="UniSTS:152565"

variation 270983
/allele="C"
/allele="A"

variation	/db_xref="dbSNP:314516" 271345 /allele="T" /allele="C"
variation	/db_xref="dbSNP:974418" 271685 /allele="T" /allele="C"
variation	/db_xref="dbSNP:314517" 274598 /allele="C" /allele="T"
variation	/db_xref="dbSNP:314481" 275490 /allele="A" /allele="C"
variation	/db_xref="dbSNP:1675339" 275508 /allele="G" /allele="T"
variation	/db_xref="dbSNP:192872" 277780 /allele="A" /allele="G"
variation	/db_xref="dbSNP:1460912" 279173 /allele="A" /allele="G"
variation	/db_xref="dbSNP:314479" 279494 /allele="G" /allele="T"
variation	/db_xref="dbSNP:973550" 279882 /allele="A" /allele="G"
variation	/db_xref="dbSNP:754173" 280870 /allele="C" /allele="G"
STS	/db_xref="dbSNP:314478" 283806..283902 /standard_name="2024"
variation	/db_xref="UniSTS:2716" 285455 /allele="C" /allele="T"
variation	/db_xref="dbSNP:314465" 285775 /allele="A" /allele="G"
variation	/db_xref="dbSNP:314466" 289129 /allele="G" /allele="A"
variation	/db_xref="dbSNP:2017217" 289278 /allele="C" /allele="T"
	/db_xref="dbSNP:314472"

variation	289435 /allele="C" /allele="T" /db_xref="dbSNP:314471"
variation	290520 /allele="C" /allele="T" /db_xref="dbSNP:314470"
STS	291021..291296 /standard_name="D11S3730" /db_xref="UniSTS:152960"
variation	291023 /allele="G" /allele="A" /db_xref="dbSNP:2048541"
variation	293992 /allele="A" /allele="C" /db_xref="dbSNP:314468"
variation	294595 /allele="G" /allele="A" /db_xref="dbSNP:314467"
variation	297404 /allele="G" /allele="A" /db_xref="dbSNP:314485"
variation	299377 /allele="A" /allele="G" /db_xref="dbSNP:314484"
variation	301111 /allele="A" /allele="G" /db_xref="dbSNP:314483"
variation	301251 /allele="A" /allele="C" /db_xref="dbSNP:314482"
variation	307568 /allele="T" /allele="G" /db_xref="dbSNP:907616"
variation	307901 /allele="T" /allele="C" /db_xref="dbSNP:907615"
variation	308048 /allele="G" /allele="A" /db_xref="dbSNP:754410"
variation	308290 /allele="T" /allele="C" /db_xref="dbSNP:754409"
variation	311583 /allele="C" /allele="T" /db_xref="dbSNP:693245"
variation	312053

	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:647992"
	316397
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:1460913"
	318487
	/allele="A"
	/allele="G"
STS	/db_xref="dbSNP:1460914"
	320845..321150
	/standard_name="SHGC-149106"
variation	/db_xref="UniSTS:176801"
	320873
	/allele="A"
	/allele="C"
variation	/db_xref="dbSNP:1380987"
	320924
	/allele="C"
	/allele="T"
STS	/db_xref="dbSNP:898614"
	321200..321461
	/standard_name="C95612"
variation	/db_xref="UniSTS:16841"
	321519
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:734992"
	322008
	/allele="C"
	/allele="G"
variation	/db_xref="dbSNP:1531368"
	322679
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:1000402"
	322746
	/allele="C"
	/allele="A"
variation	/db_xref="dbSNP:1000401"
	322866
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:1000400"
	329098
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:718484"
	329139
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:718485"
	329348
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:718486"
	329508
	/allele="T"
	/allele="C"

variation	/db_xref="dbSNP:1380988" 339180 /allele="T" /allele="C"
STS	/db_xref="dbSNP:2219600" 343886..344185 /standard_name="D11S3864" /db_xref="UniSTS:153087"
STS	344034..344133 /standard_name="C95604" /db_xref="UniSTS:75887"
variation	344973 /allele="T" /allele="C"
variation	/db_xref="dbSNP:1460911" 347363 /allele="G" /allele="A"
variation	/db_xref="dbSNP:1350762" 350509 /allele="G" /allele="A"
variation	/db_xref="dbSNP:1460910" 350640 /allele="G" /allele="C"
variation	/db_xref="dbSNP:1563901" 350676 /allele="T" /allele="C"
variation	/db_xref="dbSNP:1563900" 350701 /allele="G" /allele="A"
variation	/db_xref="dbSNP:1563899" 350880 /allele="G" /allele="A"
variation	/db_xref="dbSNP:979219" 357688 /allele="T" /allele="A"
variation	/db_xref="dbSNP:1460915" 359569 /allele="G" /allele="A"
variation	/db_xref="dbSNP:2085833" 364184 /allele="T" /allele="C"
variation	/db_xref="dbSNP:1563898" 364206 /allele="C" /allele="T"
variation	/db_xref="dbSNP:1008950" 364349 /allele="G" /allele="A"
variation	/db_xref="dbSNP:898615" 365712

variation /allele="T"
/allele="A"
/db_xref="dbSNP:922205"
366896
/allele="G"
/allele="A"
variation /db_xref="dbSNP:1563902"
367061
/allele="G"
/allele="A"
variation /db_xref="dbSNP:1008952"
367233
/allele="T"
/allele="A"
STS /db_xref="dbSNP:1008951"
378152..378483
/standard_name="C95613"
/note="WARNING: map location ambiguous"
STS /db_xref="UniSTS:6866"
378152..378255
/standard_name="C95601"
/note="WARNING: map location ambiguous"
variation /db_xref="UniSTS:6867"
382950
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
variation /db_xref="dbSNP:2157610"
386293
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
STS /db_xref="dbSNP:1648368"
390883..391138
/standard_name="D11S2337"
/note="WARNING: map location ambiguous"
STS /db_xref="UniSTS:68483"
400681..400881
/standard_name="C95573"
/note="WARNING: map location ambiguous"
variation /db_xref="UniSTS:12259"
404883
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
variation /db_xref="dbSNP:885882"
406208
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
variation /db_xref="dbSNP:2019767"
408354
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
variation /db_xref="dbSNP:756578"
420237
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"


```

      /db_xref="dbSNP:2020100"
STS      421259..421432
      /standard_name="D11S2036"
      /note="WARNING: map location ambiguous"
      /db_xref="UniSTS:73943"
variation 422403
      /note="WARNING: map location ambiguous"
      /allele="A"
      /allele="T"
      /db_xref="dbSNP:1236908"
variation 422968
      /note="WARNING: map location ambiguous"
      /allele="C"
      /allele="T"
      /db_xref="dbSNP:2073660"
variation 422971
      /note="WARNING: map location ambiguous"
      /allele="C"
      /allele="T"
      /db_xref="dbSNP:2073661"
variation 424588
      /note="WARNING: map location ambiguous"
      /allele="A"
      /allele="G"
      /db_xref="dbSNP:1236909"
variation 426407
      /note="WARNING: map location ambiguous"
      /allele="G"
      /allele="A"
      /db_xref="dbSNP:1502074"
variation 426460
      /note="WARNING: map location ambiguous"
      /allele="G"
      /allele="A"
      /db_xref="dbSNP:1502073"
variation 426612
      /note="WARNING: map location ambiguous"
      /allele="C"
      /allele="A"
      /db_xref="dbSNP:1236910"
STS      427294..427427
      /standard_name="C95608"
      /note="WARNING: map location ambiguous"
      /db_xref="UniSTS:18375"
variation 427517
      /note="WARNING: map location ambiguous"
      /allele="T"
      /allele="C"
      /db_xref="dbSNP:883881"
variation 427526
      /note="WARNING: map location ambiguous"
      /allele="G"
      /allele="A"
      /db_xref="dbSNP:883880"
STS      427536..427858
      /standard_name="SHGC-147021"
      /note="WARNING: map location ambiguous"
      /db_xref="UniSTS:175564"
variation 427994
      /note="WARNING: map location ambiguous"

```

variation /allele="G"
/allele="C"
/db_xref="dbSNP:1698188"
429043
/note="WARNING: map location ambiguous"
/allele="T"
/allele="G"
/db_xref="dbSNP:1698187"
variation 433554
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
/db_xref="dbSNP:1632434"
variation 434039
/note="WARNING: map location ambiguous"
/allele="G"
/allele="C"
/db_xref="dbSNP:1542895"
variation 435427
/note="WARNING: map location ambiguous"
/allele="G"
/allele="C"
/db_xref="dbSNP:1698183"
variation 435664
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
/db_xref="dbSNP:1784935"
variation 435748
/note="WARNING: map location ambiguous"
/allele="A"
/allele="T"
/db_xref="dbSNP:1784936"
variation 435869
/note="WARNING: map location ambiguous"
/allele="A"
/allele="T"
/db_xref="dbSNP:1784937"
variation 436498
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:1698181"
variation 442665
/allele="C"
/allele="G"
/db_xref="dbSNP:2054311"
variation 444050
/allele="A"
/allele="C"
/db_xref="dbSNP:976946"
variation 444071
/allele="A"
/allele="G"
/db_xref="dbSNP:976947"
STS 444753..444899
/standard_name="D11S2077"
/db_xref="UniSTS:150035"
variation 453658
/allele="C"

variation /allele="T"
/db_xref="dbSNP:2126069"
457608
/allele="C"
/allele="T"
variation /db_xref="dbSNP:2126070"
458991
/allele="A"
/allele="G"
variation /db_xref="dbSNP:898613"
470116
/allele="T"
/allele="C"
variation /db_xref="dbSNP:1893165"
470129
/allele="T"
/allele="C"
STS /db_xref="dbSNP:1893164"
472049..472281
/standard_name="C95611"
/db_xref="UniSTS:66544"
variation 472364
/allele="G"
/allele="A"
variation /db_xref="dbSNP:2155640"
472956
/allele="T"
/allele="C"
variation /db_xref="dbSNP:2155639"
473091
/allele="T"
/allele="C"
variation /db_xref="dbSNP:2155638"
473533
/allele="C"
/allele="A"
variation /db_xref="dbSNP:2155637"
474822
/allele="C"
/allele="A"
variation /db_xref="dbSNP:2155636"
474881
/allele="T"
/allele="C"
variation /db_xref="dbSNP:2155635"
474958
/allele="T"
/allele="C"
variation /db_xref="dbSNP:2155634"
479117
/allele="T"
/allele="C"
variation /db_xref="dbSNP:2155633"
479138
/allele="T"
/allele="C"
variation /db_xref="dbSNP:2155632"
479346
/allele="T"
/allele="C"

variation	/db_xref="dbSNP:2186873" 482078 /allele="C" /allele="A"
variation	/db_xref="dbSNP:2155631" 487620 /allele="C" /allele="A"
variation	/db_xref="dbSNP:2212582" 487637 /allele="G" /allele="A"
variation	/db_xref="dbSNP:2212581" 488299 /allele="G" /allele="A"
variation	/db_xref="dbSNP:1785023" 488423 /allele="T" /allele="C"
variation	/db_xref="dbSNP:1785022" 488810 /allele="T" /allele="C"
variation	/db_xref="dbSNP:1785021" 490839 /allele="T" /allele="C"
variation	/db_xref="dbSNP:1698191" 491053 /allele="G" /allele="A"
variation	/db_xref="dbSNP:1785020" 492375 /allele="T" /allele="C"
variation	/db_xref="dbSNP:1785019" 492386 /allele="T" /allele="C"
variation	/db_xref="dbSNP:1698190" 492495 /allele="C" /allele="A"
variation	/db_xref="dbSNP:1698189" 493565 /allele="G" /allele="C"
variation	/db_xref="dbSNP:1785018" 494486 /allele="T" /allele="C"
variation	/db_xref="dbSNP:1698199" 495243 /allele="T" /allele="A"
STS	/db_xref="dbSNP:1785017" 495342..495544 /standard_name="KAM25" /db_xref="UniSTS:94205"

variation 495610
/allele="T"
/allele="C"
/db_xref="dbSNP:1785016"

variation 496258
/allele="T"
/allele="A"
/db_xref="dbSNP:1618710"

STS 496521..496637
/standard_name="D11S1853"
/db_xref="UniSTS:148927"

variation 497300
/allele="T"
/allele="C"
/db_xref="dbSNP:1698198"

STS 497768..497922
/standard_name="SHGC-53175"
/db_xref="UniSTS:82744"

variation 498526
/allele="T"
/allele="G"
/db_xref="dbSNP:1698197"

variation 498985
/allele="T"
/allele="C"
/db_xref="dbSNP:1698196"

variation 499325
/allele="T"
/allele="G"
/db_xref="dbSNP:1698195"

variation 499448
/allele="G"
/allele="C"
/db_xref="dbSNP:1698194"

variation 500441
/allele="T"
/allele="C"
/db_xref="dbSNP:1698192"

variation 501165
/allele="G"
/allele="C"
/db_xref="dbSNP:1785014"

variation 501990
/allele="A"
/allele="C"
/db_xref="dbSNP:1698157"

variation 502184
/allele="T"
/allele="C"
/db_xref="dbSNP:1785013"

variation 502878
/allele="G"
/allele="A"
/db_xref="dbSNP:1785011"

variation 503633
/allele="C"
/allele="G"
/db_xref="dbSNP:1698178"

variation 503719
/allele="A"

variation /allele="G"
/db_xref="dbSNP:1698182"
503969
/allele="A"
/allele="G"
variation /db_xref="dbSNP:1698184"
504194
/allele="A"
/allele="G"
variation /db_xref="dbSNP:1698185"
505367
/allele="C"
/allele="T"
variation /db_xref="dbSNP:1698206"
506329
/allele="A"
/allele="G"
variation /db_xref="dbSNP:1698207"
506490
/allele="G"
/allele="C"
variation /db_xref="dbSNP:1785010"
506559
/allele="A"
/allele="T"
STS /db_xref="dbSNP:884182"
506696..507042
/standard_name="SHGC-147706"
variation /db_xref="UniSTS:175962"
507064
/allele="T"
/allele="C"
variation /db_xref="dbSNP:1785008"
507567
/allele="A"
/allele="G"
variation /db_xref="dbSNP:1698208"
507888
/allele="G"
/allele="C"
variation /db_xref="dbSNP:1785007"
508052
/allele="T"
/allele="C"
variation /db_xref="dbSNP:1785006"
509390
/allele="C"
/allele="G"
variation /db_xref="dbSNP:1698209"
509516
/allele="G"
/allele="T"
variation /db_xref="dbSNP:1698210"
512186
/allele="G"
/allele="C"
variation /db_xref="dbSNP:1785005"
512281
/allele="C"
/allele="A"

variation /db_xref="dbSNP:1785004"
512988
/allele="G"
/allele="T"
variation /db_xref="dbSNP:1910096"
513093
/allele="C"
/allele="A"
variation /db_xref="dbSNP:2212580"
513095
/allele="C"
/allele="A"
variation /db_xref="dbSNP:2212579"
513125
/allele="G"
/allele="T"
variation /db_xref="dbSNP:1910097"
513991
/allele="C"
/allele="T"
variation /db_xref="dbSNP:1698211"
514482
/allele="G"
/allele="C"
variation /db_xref="dbSNP:1785003"
514495
/allele="G"
/allele="A"
variation /db_xref="dbSNP:1785002"
514521
/allele="T"
/allele="A"
variation /db_xref="dbSNP:1785001"
514794
/allele="G"
/allele="T"
variation /db_xref="dbSNP:1629035"
515051
/allele="G"
/allele="A"
variation /db_xref="dbSNP:1785000"
515414
/allele="C"
/allele="T"
variation /db_xref="dbSNP:1698212"
516254
/allele="T"
/allele="C"
variation /db_xref="dbSNP:1784999"
516494
/allele="T"
/allele="C"
variation /db_xref="dbSNP:1784998"
516792
/allele="A"
/allele="G"
variation /db_xref="dbSNP:1502077"
517604
/allele="G"
/allele="C"

variation	/db_xref="dbSNP:1784997" 517802 /allele="G" /allele="A"
variation	/db_xref="dbSNP:1784996" 517847 /allele="A" /allele="G"
variation	/db_xref="dbSNP:1698213" 518546 /allele="C" /allele="T"
variation	/db_xref="dbSNP:1502078" 518572 /allele="C" /allele="T"
variation	/db_xref="dbSNP:1502079" 518579 /allele="T" /allele="C"
variation	/db_xref="dbSNP:1784995" 518596 /allele="C" /allele="T"
variation	/db_xref="dbSNP:1847088" 518757 /allele="C" /allele="T"
variation	/db_xref="dbSNP:1039445" 518925 /allele="A" /allele="G"
variation	/db_xref="dbSNP:1039446" 520079 /allele="G" /allele="C"
variation	/db_xref="dbSNP:1784994" 520898 /allele="C" /allele="A"
variation	/db_xref="dbSNP:1698204" 521347 /allele="A" /allele="G"
variation	/db_xref="dbSNP:885322" 521493 /allele="C" /allele="T"
variation	/db_xref="dbSNP:885323" 522027 /allele="T" /allele="C"
variation	/db_xref="dbSNP:1698200" 522052 /allele="G" /allele="A"
variation	/db_xref="dbSNP:1784992" 522179 /allele="G" /allele="A"

variation /db_xref="dbSNP:1784991"
522441
/allele="C"
/allele="A"
variation /db_xref="dbSNP:1784990"
522921
/allele="G"
/allele="C"
variation /db_xref="dbSNP:1784989"
523217
/allele="T"
/allele="C"
variation /db_xref="dbSNP:1502076"
523390
/allele="G"
/allele="C"
variation /db_xref="dbSNP:1502075"
523723
/allele="T"
/allele="A"
variation /db_xref="dbSNP:1784988"
525255
/allele="G"
/allele="A"
variation /db_xref="dbSNP:1616116"
525640
/allele="T"
/allele="C"
variation /db_xref="dbSNP:1612635"
526743
/allele="G"
/allele="C"
variation /db_xref="dbSNP:1784987"
527030
/allele="T"
/allele="C"
variation /db_xref="dbSNP:1698205"
527052
/allele="T"
/allele="C"
variation /db_xref="dbSNP:1784986"
527242
/allele="T"
/allele="C"
variation /db_xref="dbSNP:905247"
527674
/allele="T"
/allele="C"
variation /db_xref="dbSNP:1784985"
527879
/allele="G"
/allele="C"
variation /db_xref="dbSNP:1698203"
527949
/allele="G"
/allele="A"
variation /db_xref="dbSNP:1784984"
528207
/allele="G"
/allele="A"

variation /db_xref="dbSNP:1784983"
528410
/allele="G"
/allele="A"

STS /db_xref="dbSNP:1784982"
528587..528910
/standard_name="SHGC-148942"
/db_xref="UniSTS:176695"

variation 528710
/allele="A"
/allele="G"

variation /db_xref="dbSNP:884653"
528713
/allele="C"
/allele="T"

variation /db_xref="dbSNP:884654"
528814
/allele="C"
/allele="T"

variation /db_xref="dbSNP:867272"
529294
/allele="G"
/allele="C"

variation /db_xref="dbSNP:1784980"
531018
/allele="G"
/allele="A"

variation /db_xref="dbSNP:1784979"
531155
/allele="G"
/allele="C"

variation /db_xref="dbSNP:1784978"
531207
/allele="T"
/allele="C"

variation /db_xref="dbSNP:1784977"
532188
/allele="G"
/allele="A"

variation /db_xref="dbSNP:1625168"
532265
/allele="T"
/allele="C"

variation /db_xref="dbSNP:1784976"
533202
/allele="G"
/allele="A"

variation /db_xref="dbSNP:1619714"
534256
/allele="G"
/allele="A"

variation /db_xref="dbSNP:1784975"
535799
/allele="T"
/allele="A"

variation /db_xref="dbSNP:1698202"
538251
/allele="G"
/allele="A"

variation /db_xref="dbSNP:1784973"

variation 539053
/allele="G"
/allele="A"
/db_xref="dbSNP:1625713"

variation 539670
/allele="T"
/allele="G"
/db_xref="dbSNP:1784972"

variation 540447
/allele="A"
/allele="G"
/db_xref="dbSNP:1698143"

variation 540468
/allele="A"
/allele="G"
/db_xref="dbSNP:1393273"

variation 540650
/allele="C"
/allele="G"
/db_xref="dbSNP:1698144"

variation 541856
/allele="G"
/allele="C"
/db_xref="dbSNP:1784971"

variation 542909
/allele="G"
/allele="A"
/db_xref="dbSNP:1784970"

variation 543230
/allele="T"
/allele="C"
/db_xref="dbSNP:1784969"

variation 543255
/allele="G"
/allele="C"
/db_xref="dbSNP:1784968"

variation 543514
/allele="T"
/allele="C"
/db_xref="dbSNP:1784967"

variation 543530
/allele="T"
/allele="C"
/db_xref="dbSNP:1784966"

variation 543717
/allele="T"
/allele="C"
/db_xref="dbSNP:1784965"

variation 543839
/allele="G"
/allele="A"
/db_xref="dbSNP:1784964"

variation 544550
/allele="A"
/allele="G"
/db_xref="dbSNP:1616382"

variation 544679
/allele="A"
/allele="C"
/db_xref="dbSNP:2088930"

variation 544828
/allele="C"
/allele="T"
/db_xref="dbSNP:2102156"

variation 545184
/allele="A"
/allele="G"
/db_xref="dbSNP:1910095"

variation 545715
/allele="A"
/allele="G"
/db_xref="dbSNP:1698147"

variation 545886
/allele="G"
/allele="A"
/db_xref="dbSNP:1784961"

STS 546357..546615
/standard_name="D11S1136"
/db_xref="UniSTS:52418"

variation 546410
/allele="A"
/allele="G"
/db_xref="dbSNP:1698148"

variation 546828
/allele="A"
/allele="T"
/db_xref="dbSNP:878650"

variation 546860
/allele="A"
/allele="G"
/db_xref="dbSNP:905244"

variation 547810
/allele="T"
/allele="C"
/db_xref="dbSNP:1784960"

variation 548339
/allele="G"
/allele="A"
/db_xref="dbSNP:1784959"

variation 548452
/allele="C"
/allele="T"
/db_xref="dbSNP:1698149"

variation 548938
/allele="A"
/allele="C"
/db_xref="dbSNP:1110361"

variation 549046
/allele="G"
/allele="A"
/db_xref="dbSNP:1784958"

variation 549212
/allele="A"
/allele="G"
/db_xref="dbSNP:885259"

variation 549623
/allele="G"
/allele="T"
/db_xref="dbSNP:1698151"

variation 549773

variation /allele="C"
/allele="T"
/db_xref="dbSNP:905245"
550093
/allele="C"
/allele="T"
/db_xref="dbSNP:883436"
STS 550320..550663
/standard_name="SHGC-145924"
/db_xref="UniSTS:174882"
variation 550350
/allele="A"
/allele="G"
/db_xref="dbSNP:905246"
STS 550456..550777
/standard_name="SHGC-145874"
/db_xref="UniSTS:174848"
variation 550483
/allele="C"
/allele="T"
/db_xref="dbSNP:975027"
variation 550824
/allele="G"
/allele="A"
/db_xref="dbSNP:883419"
variation 551229
/allele="C"
/allele="T"
/db_xref="dbSNP:872726"
STS 551230..551532
/standard_name="SHGC-156235"
/db_xref="UniSTS:182473"
variation 551369
/allele="A"
/allele="G"
/db_xref="dbSNP:883256"
variation 551410
/allele="C"
/allele="T"
/db_xref="dbSNP:872727"
variation 551992
/allele="G"
/allele="A"
/db_xref="dbSNP:868365"
variation 552001
/allele="G"
/allele="T"
/db_xref="dbSNP:1502072"
variation 552376
/allele="C"
/allele="G"
/db_xref="dbSNP:1698158"
variation 552506
/allele="G"
/allele="T"
/db_xref="dbSNP:1698159"
variation 552728
/allele="T"
/allele="C"
/db_xref="dbSNP:1614130"

variation 552897
/allele="C"
/allele="G"
/db_xref="dbSNP:1698160"

variation 552971
/allele="G"
/allele="A"
/db_xref="dbSNP:1784956"

variation 553262
/allele="G"
/allele="T"
/db_xref="dbSNP:1698161"

variation 553302
/allele="G"
/allele="A"
/db_xref="dbSNP:1784955"

variation 553405
/allele="A"
/allele="C"
/db_xref="dbSNP:1698162"

variation 553690
/allele="A"
/allele="G"
/db_xref="dbSNP:1698163"

variation 553952
/allele="C"
/allele="T"
/db_xref="dbSNP:971374"

variation 554009
/allele="C"
/allele="T"
/db_xref="dbSNP:971375"

variation 554088
/allele="C"
/allele="T"
/db_xref="dbSNP:971376"

variation 554127
/allele="A"
/allele="G"
/db_xref="dbSNP:971377"

variation 554484
/allele="C"
/allele="G"
/db_xref="dbSNP:2019748"

variation 554550
/allele="T"
/allele="C"
/db_xref="dbSNP:1784953"

variation 554807
/allele="C"
/allele="T"
/db_xref="dbSNP:1698166"

variation 554846
/allele="A"
/allele="G"
/db_xref="dbSNP:1698167"

variation 554884
/allele="T"
/allele="G"
/db_xref="dbSNP:1784952"

variation	554907
	/allele="A"
	/allele="C"
	/db_xref="dbSNP:1698168"
variation	554945
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:1698169"
variation	555945
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:1784951"
variation	556214
	/allele="T"
	/allele="G"
	/db_xref="dbSNP:1784950"
variation	556486
	/allele="T"
	/allele="A"
	/db_xref="dbSNP:1784949"
variation	556923
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:1784948"
variation	557048
	/allele="T"
	/allele="G"
	/db_xref="dbSNP:1784947"
variation	557239
	/allele="T"
	/allele="A"
	/db_xref="dbSNP:1784946"
variation	557307
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:1698171"
variation	557373
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:1784945"
variation	558030
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:1784944"
variation	558031
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:1626242"
variation	558481
	/allele="G"
	/allele="C"
	/db_xref="dbSNP:1620956"
variation	558548
	/allele="C"
	/allele="A"
	/db_xref="dbSNP:1620779"
variation	558783
	/allele="G"
	/allele="C"
	/db_xref="dbSNP:1618400"

variation 559102
/allele="T"
/allele="A"
/db_xref="dbSNP:1615833"

variation 559336
/allele="A"
/allele="T"
/db_xref="dbSNP:1027648"

variation 559347
/allele="C"
/allele="T"
/db_xref="dbSNP:1016853"

variation 559423
/allele="C"
/allele="G"
/db_xref="dbSNP:2173985"

variation 559778
/allele="G"
/allele="A"
/db_xref="dbSNP:1784943"

variation 560244
/allele="T"
/allele="C"
/db_xref="dbSNP:1784942"

variation 560269
/allele="A"
/allele="G"
/db_xref="dbSNP:1698173"

variation 560281
/allele="T"
/allele="C"
/db_xref="dbSNP:1784941"

variation 560760
/allele="T"
/allele="C"
/db_xref="dbSNP:1784940"

variation 560974
/allele="G"
/allele="A"
/db_xref="dbSNP:1784939"

variation 561669
/allele="T"
/allele="C"
/db_xref="dbSNP:1784938"

variation 566468
/allele="G"
/allele="T"
/db_xref="dbSNP:1698174"

variation 567027
/allele="G"
/allele="A"
/db_xref="dbSNP:1698175"

variation 567300
/allele="G"
/allele="C"
/db_xref="dbSNP:1698176"

variation 567526
/allele="A"
/allele="T"
/db_xref="dbSNP:1698177"

variation 568507
/allele="C"
/allele="G"
/db_xref="dbSNP:1698179"

variation 568658
/allele="G"
/allele="T"
/db_xref="dbSNP:1698180"

variation 568774
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
/db_xref="dbSNP:1698181"

variation 569398
/note="WARNING: map location ambiguous"
/allele="T"
/allele="A"
/db_xref="dbSNP:1784937"

variation 569519
/note="WARNING: map location ambiguous"
/allele="T"
/allele="A"
/db_xref="dbSNP:1784936"

variation 569603
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:1784935"

variation 569840
/note="WARNING: map location ambiguous"
/allele="C"
/allele="G"
/db_xref="dbSNP:1698183"

variation 571228
/note="WARNING: map location ambiguous"
/allele="C"
/allele="G"
/db_xref="dbSNP:1542895"

variation 571713
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:1632434"

variation 576224
/note="WARNING: map location ambiguous"
/allele="A"
/allele="C"
/db_xref="dbSNP:1698187"

variation 577272
/note="WARNING: map location ambiguous"
/allele="C"
/allele="G"
/db_xref="dbSNP:1698188"

STS 577408..577730
/standard_name="SHGC-147021"
/note="WARNING: map location ambiguous"
/db_xref="UniSTS:175564"

variation 577740
/note="WARNING: map location ambiguous"
/allele="C"

```

/allele="T"
/db_xref="dbSNP:883880"
variation 577749
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
/db_xref="dbSNP:883881"
STS 577839..577972
/standard_name="C95608"
/note="WARNING: map location ambiguous"
/db_xref="UniSTS:18375"
variation 578654
/note="WARNING: map location ambiguous"
/allele="G"
/allele="T"
/db_xref="dbSNP:1236910"
variation 578806
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
/db_xref="dbSNP:1502073"
variation 578859
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
/db_xref="dbSNP:1502074"
variation 580677
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:1236909"
variation 582294
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:2073661"
variation 582297
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:2073660"
variation 582861
/note="WARNING: map location ambiguous"
/allele="T"
/allele="A"
/db_xref="dbSNP:1236908"
STS 583832..584005
/standard_name="D11S2036"
/note="WARNING: map location ambiguous"
/db_xref="UniSTS:73943"
variation 585027
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:2020100"
variation 589175
/allele="T"
/allele="C"
/db_xref="dbSNP:733072"
STS 599989..600244

```

STS
/standard_name="D11S2337"
/note="WARNING: map location ambiguous"
/db_xref="UniSTS:68483"
609787..609987
/standard_name="C95573"
/note="WARNING: map location ambiguous"
/db_xref="UniSTS:12259"
variation
613989
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:885882"
variation
615314
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
/db_xref="dbSNP:2019767"
variation
617460
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:756578"
STS
630976..631131
/standard_name="D11S1992"
/db_xref="UniSTS:74797"
variation
635706
/allele="T"
/allele="C"
/db_xref="dbSNP:1393275"
variation
635962
/allele="T"
/allele="C"
/db_xref="dbSNP:1393274"
STS
646481..646732
/standard_name="C95607"
/db_xref="UniSTS:48717"
variation
667970
/allele="A"
/allele="G"
/db_xref="dbSNP:1939682"
variation
669054
/allele="C"
/allele="T"
/db_xref="dbSNP:1939683"
variation
672316
/allele="G"
/allele="A"
/db_xref="dbSNP:1939678"
variation
684377
/allele="T"
/allele="C"
/db_xref="dbSNP:2155276"
variation
684508
/allele="G"
/allele="C"
/db_xref="dbSNP:2155275"
variation
689088
/allele="G"
/allele="T"
/db_xref="dbSNP:1892977"

STS 691105..691236
/standard_name="D11S2079"
/db_xref="UniSTS:150036"

variation 692743
/allele="T"
/allele="G"
/db_xref="dbSNP:1939684"

variation 694690
/allele="T"
/allele="A"
/db_xref="dbSNP:2000574"

variation 696400
/allele="T"
/allele="C"
/db_xref="dbSNP:1939679"

variation 698334
/allele="T"
/allele="G"
/db_xref="dbSNP:948037"

variation 698778
/allele="C"
/allele="A"
/db_xref="dbSNP:2008979"

variation 699173
/allele="T"
/allele="C"
/db_xref="dbSNP:1939693"

variation 700571
/allele="G"
/allele="A"
/db_xref="dbSNP:1939692"

variation 712994
/allele="C"
/allele="G"
/db_xref="dbSNP:1939680"

variation 713269
/allele="A"
/allele="G"
/db_xref="dbSNP:1939681"

variation 713802
/allele="C"
/allele="T"
/db_xref="dbSNP:2155269"

variation 713939
/allele="A"
/allele="T"
/db_xref="dbSNP:2155270"

variation 713967
/allele="A"
/allele="G"
/db_xref="dbSNP:2155271"

variation 713984
/allele="C"
/allele="T"
/db_xref="dbSNP:2155272"

variation 723075
/allele="T"
/allele="C"
/db_xref="dbSNP:1939691"

variation 723131

```

/allele="C"
/allele="T"
/db_xref="dbSNP:719187"
variation 723390
/allele="G"
/allele="C"
/db_xref="dbSNP:1939690"
variation 732114
/allele="T"
/allele="C"
/db_xref="dbSNP:585008"
variation 733354
/allele="C"
/allele="A"
/db_xref="dbSNP:569462"
variation 738788
/allele="C"
/allele="A"
/db_xref="dbSNP:546159"
STS 739991..740140
/standard_name="C95609"
/db_xref="UniSTS:40222"
variation 740784
/allele="T"
/allele="G"
/db_xref="dbSNP:2186703"
variation 740955
/allele="G"
/allele="A"
/db_xref="dbSNP:651667"
variation 741279
/allele="G"
/allele="C"
/db_xref="dbSNP:639930"
variation 741442
/allele="T"
/allele="C"
/db_xref="dbSNP:639053"
variation 742454
/allele="T"
/allele="A"
/db_xref="dbSNP:1939689"
variation 743963
/allele="T"
/allele="C"
/db_xref="dbSNP:640348"
variation 744153
/allele="G"
/allele="C"
/db_xref="dbSNP:639791"
variation 744322
/allele="T"
/allele="C"
/db_xref="dbSNP:638882"
variation 744763
/allele="G"
/allele="A"
/db_xref="dbSNP:543840"
variation 746375
/allele="C"

```

	/allele="A"
	/db_xref="dbSNP:609069"
variation	746643
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:531253"
variation	746965
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:1239111"
variation	747132
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:595450"
variation	747313
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:594573"
variation	747846
	/allele="C"
	/allele="A"
	/db_xref="dbSNP:477888"
variation	747848
	/allele="C"
	/allele="A"
	/db_xref="dbSNP:477886"
variation	748065
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:693246"
variation	748436
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:2155268"
variation	748501
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:2155267"
variation	748533
	/allele="C"
	/allele="A"
	/db_xref="dbSNP:2155266"
variation	748647
	/allele="G"
	/allele="C"
	/db_xref="dbSNP:675909"
variation	749501
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:563665"
variation	749747
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:561631"
variation	753400
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:649942"
variation	755337
	/allele="A"

variation /allele="C"
/db_xref="dbSNP:1892976"
755973
/allele="T"
/allele="C"
variation /db_xref="dbSNP:1939871"
758870
/allele="C"
/allele="T"
variation /db_xref="dbSNP:1939685"
759392
/allele="T"
/allele="G"
variation /db_xref="dbSNP:2186735"
759441
/allele="T"
/allele="G"
variation /db_xref="dbSNP:2155351"
759476
/allele="G"
/allele="A"
variation /db_xref="dbSNP:2155350"
759713
/allele="G"
/allele="A"
variation /db_xref="dbSNP:2155349"
760446
/allele="T"
/allele="A"
variation /db_xref="dbSNP:1893012"
763214
/allele="A"
/allele="T"
STS /db_xref="dbSNP:2155273"
763751..763877
/standard_name="SHGC-132169"
/db_xref="UniSTS:170690"
STS 763751..763877
/standard_name="SHGC-14502"
/db_xref="UniSTS:29772"
variation 764177
/allele="G"
/allele="A"
variation /db_xref="dbSNP:1939870"
765633
/allele="A"
/allele="G"
variation /db_xref="dbSNP:1939686"
765700
/allele="C"
/allele="T"
variation /db_xref="dbSNP:1939687"
765712
/allele="A"
/allele="G"
variation /db_xref="dbSNP:1939688"
767781
/allele="G"
/allele="C"
/db_xref="dbSNP:948074"

variation 767782
/allele="C"
/allele="A"
/db_xref="dbSNP:948073"

variation 768584
/allele="A"
/allele="T"
/db_xref="dbSNP:1320650"

variation 768704
/allele="C"
/allele="A"
/db_xref="dbSNP:1320654"

variation 768814
/allele="G"
/allele="C"
/db_xref="dbSNP:948072"

STS 769645..769841
/standard_name="C95584"
/db_xref="UniSTS:54197"

variation 769794
/allele="T"
/allele="C"
/db_xref="dbSNP:1784261"

variation 770005
/allele="A"
/allele="G"
/db_xref="dbSNP:1271759"

variation 770155
/allele="G"
/allele="A"
/db_xref="dbSNP:1268309"

variation 770765
/allele="C"
/allele="A"
/db_xref="dbSNP:1262591"

variation 770911
/allele="T"
/allele="C"
/db_xref="dbSNP:1632800"

variation 771202
/allele="T"
/allele="C"
/db_xref="dbSNP:1784260"

variation 771495
/allele="C"
/allele="T"
/db_xref="dbSNP:1262592"

variation 771628
/allele="C"
/allele="T"
/db_xref="dbSNP:1262593"

variation 771722
/allele="A"
/allele="T"
/db_xref="dbSNP:435472"

variation 771782
/allele="A"
/allele="T"
/db_xref="dbSNP:417220"

variation 771811

	/allele="A"
	/allele="T"
variation	/db_xref="dbSNP:1145178"
	771866
	/allele="A"
	/allele="T"
variation	/db_xref="dbSNP:454918"
	771895
	/allele="A"
	/allele="T"
STS	/db_xref="dbSNP:1145179"
	772237..772390
	/standard_name="C95629"
	/db_xref="UniSTS:2440"
variation	772387
	/allele="G"
	/allele="T"
variation	/db_xref="dbSNP:574633"
	772526
	/allele="A"
	/allele="T"
variation	/db_xref="dbSNP:436886"
	773052
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:374729"
	773093
	/allele="C"
	/allele="A"
variation	/db_xref="dbSNP:637121"
	773483
	/allele="G"
	/allele="T"
variation	/db_xref="dbSNP:431911"
	774071
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:622631"
	774841
	/allele="C"
	/allele="G"
variation	/db_xref="dbSNP:411036"
	775086
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:435016"
	775183
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:120561"
	775470
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:400189"
	776014
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:400191"
	777348
	/allele="A"

variation /allele="G"
/db_xref="dbSNP:445378"
777838
/allele="C"
/allele="T"
/db_xref="dbSNP:2157609"
variation 780595
/allele="G"
/allele="A"
/db_xref="dbSNP:1939869"
variation 780890
/allele="C"
/allele="G"
/db_xref="dbSNP:429849"
variation 781422
/allele="C"
/allele="G"
/db_xref="dbSNP:393716"
variation 782208
/allele="C"
/allele="G"
/db_xref="dbSNP:387626"
variation 782718
/allele="C"
/allele="T"
/db_xref="dbSNP:367164"
variation 783479
/allele="C"
/allele="T"
/db_xref="dbSNP:369845"
variation 784203
/allele="A"
/allele="C"
/db_xref="dbSNP:427875"
variation 784254
/allele="A"
/allele="G"
/db_xref="dbSNP:420087"
STS 784932..785217
/standard_name="C95614"
/db_xref="UniSTS:63368"
variation 787566
/allele="A"
/allele="T"
/db_xref="dbSNP:445033"
variation 788641
/allele="C"
/allele="T"
/db_xref="dbSNP:453838"
variation 788911
/allele="A"
/allele="G"
/db_xref="dbSNP:404138"
variation 788955
/allele="A"
/allele="G"
/db_xref="dbSNP:436275"
variation 789255
/allele="C"
/allele="G"

variation	/db_xref="dbSNP:446253" 790159 /allele="C" /allele="T"
variation	/db_xref="dbSNP:405667" 790234 /allele="C" /allele="T"
variation	/db_xref="dbSNP:435864" 791308 /allele="G" /allele="T"
variation	/db_xref="dbSNP:441211" 792448 /allele="A" /allele="G"
variation	/db_xref="dbSNP:1145180" 792502 /allele="C" /allele="T"
variation	/db_xref="dbSNP:400639" 794349 /allele="C" /allele="T"
variation	/db_xref="dbSNP:1784211" 794377 /allele="C" /allele="T"
variation	/db_xref="dbSNP:1784212" 794387 /allele="C" /allele="T"
variation	/db_xref="dbSNP:1144032" 797731 /allele="A" /allele="G"
variation	/db_xref="dbSNP:424989" 797781 /allele="C" /allele="A"
variation	/db_xref="dbSNP:641124" 797855 /allele="C" /allele="A"
variation	/db_xref="dbSNP:651886" 798292 /allele="G" /allele="A"
variation	/db_xref="dbSNP:434881" 798480 /allele="C" /allele="T"
variation	/db_xref="dbSNP:379878" 799520 /allele="A" /allele="T"
variation	/db_xref="dbSNP:375230" 799941 /allele="A" /allele="G"

variation /db_xref="dbSNP:446815"
799988
/allele="C"
/allele="T"
/db_xref="dbSNP:415505"
variation 801916
/allele="C"
/allele="T"
/db_xref="dbSNP:422456"
variation 803132
/allele="C"
/allele="T"
/db_xref="dbSNP:1144033"
variation 803373
/allele="C"
/allele="T"
/db_xref="dbSNP:1145181"
variation 803585
/allele="A"
/allele="G"
/db_xref="dbSNP:1145182"
variation 803795
/allele="A"
/allele="G"
/db_xref="dbSNP:976918"
variation 804236
/allele="C"
/allele="G"
/db_xref="dbSNP:371157"
variation 805294
/allele="A"
/allele="G"
/db_xref="dbSNP:372453"
variation 805334
/allele="G"
/allele="A"
/db_xref="dbSNP:547700"
variation 807763
/allele="C"
/allele="T"
/db_xref="dbSNP:1076141"
variation 812032
/allele="A"
/allele="C"
/db_xref="dbSNP:498269"
STS 813760..813890
/standard_name="C95610"
/db_xref="UniSTS:69736"
variation 816909
/allele="T"
/allele="C"
/db_xref="dbSNP:877601"
STS 816932..817039
/standard_name="D11S4367"
/db_xref="UniSTS:74906"
STS 826748..826954
/standard_name="D11S4111"
/db_xref="UniSTS:24818"
variation 832221
/allele="T"

/allele="G"
/db_xref="dbSNP:1030393"
STS 834268..834461
/standard_name="D11S3552"
/db_xref="UniSTS:152791"
variation 835357
/allele="G"
/allele="T"
/db_xref="dbSNP:1262514"
variation 843450
/allele="G"
/allele="T"
/db_xref="dbSNP:1632803"
STS 843684..843863
/standard_name="C95592"
/db_xref="UniSTS:72741"
variation 846703
/allele="T"
/allele="C"
/db_xref="dbSNP:396046"
variation 856046
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
/db_xref="dbSNP:2157610"
STS 862405..862736
/standard_name="C95613"
/note="WARNING: map location ambiguous"
/db_xref="UniSTS:6866"
STS 862633..862736
/standard_name="C95601"
/note="WARNING: map location ambiguous"
/db_xref="UniSTS:6867"
variation 873202
/allele="T"
/allele="G"
/db_xref="dbSNP:1791897"
variation 874078
/allele="C"
/allele="A"
/db_xref="dbSNP:1632795"
variation 874206
/allele="T"
/allele="G"
/db_xref="dbSNP:1648372"
variation 874227
/allele="T"
/allele="C"
/db_xref="dbSNP:1648371"
variation 874298
/allele="G"
/allele="A"
/db_xref="dbSNP:1648370"
variation 876778
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:1648368"
variation 880678
/allele="T"

variation /allele="C"
/db_xref="dbSNP:1612750"
882885
/allele="C"
/allele="G"
variation /db_xref="dbSNP:1791917"
883097
/allele="A"
/allele="T"
variation /db_xref="dbSNP:2156800"
884637
/allele="C"
/allele="G"
variation /db_xref="dbSNP:400068"
884865
/allele="C"
/allele="T"
variation /db_xref="dbSNP:410045"
884924
/allele="C"
/allele="T"
variation /db_xref="dbSNP:372064"
885101
/allele="C"
/allele="T"
variation /db_xref="dbSNP:404693"
885406
/allele="C"
/allele="T"
variation /db_xref="dbSNP:411374"
885425
/allele="A"
/allele="G"
STS /db_xref="dbSNP:400831"
885798..886018
/standard_name="D11S1256"
/db_xref="UniSTS:148349"
variation 885908
/allele="A"
/allele="G"
variation /db_xref="dbSNP:1632798"
886802
/allele="A"
/allele="C"
variation /db_xref="dbSNP:403926"
886911
/allele="G"
/allele="T"
variation /db_xref="dbSNP:384464"
886981
/allele="G"
/allele="T"
variation /db_xref="dbSNP:379625"
887023
/allele="C"
/allele="T"
variation /db_xref="dbSNP:375724"
887709
/allele="C"
/allele="T"

variation	/db_xref="dbSNP:431736" 888125 /allele="A" /allele="G"
variation	/db_xref="dbSNP:387401" 890180 /allele="T" /allele="C"
variation	/db_xref="dbSNP:400096" 891868 /allele="A" /allele="G"
variation	/db_xref="dbSNP:1945387" 891881 /allele="A" /allele="G"
variation	/db_xref="dbSNP:1945388" 896342 /allele="G" /allele="T"
variation	/db_xref="dbSNP:1791915" 896690 /allele="C" /allele="G"
variation	/db_xref="dbSNP:406641" 897588 /allele="C" /allele="T"
variation	/db_xref="dbSNP:930005" 898551 /allele="C" /allele="G"
variation	/db_xref="dbSNP:1632799" 899687 /allele="C" /allele="T"
variation	/db_xref="dbSNP:429795" 900534 /allele="A" /allele="G"
STS	/db_xref="dbSNP:1632801" 900545..900889 /standard_name="SHGC-78632"
STS	/db_xref="UniSTS:102088" 901031..901238 /standard_name="C95585"
variation	/db_xref="UniSTS:18129" 903026 /allele="G" /allele="A"
variation	/db_xref="dbSNP:890424" 903037 /allele="A" /allele="G"
variation	/db_xref="dbSNP:730898" 903778 /allele="A" /allele="G"
variation	/db_xref="dbSNP:1648358" 904664

	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:1791916"
	913474
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:1991302"
	913936
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:1557451"
	914491
	/allele="T"
	/allele="A"
variation	/db_xref="dbSNP:736287"
	915004
	/allele="A"
	/allele="T"
variation	/db_xref="dbSNP:1648379"
	915958
	/allele="C"
	/allele="A"
variation	/db_xref="dbSNP:1620220"
	915959
	/allele="C"
	/allele="A"
variation	/db_xref="dbSNP:1620190"
	916107
	/allele="T"
	/allele="C"
variation	/db_xref="dbSNP:1619240"
	917481
	/allele="A"
	/allele="C"
variation	/db_xref="dbSNP:1648355"
	918712
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:1991301"
	921847
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:720037"
	921885
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:1791902"
	921981
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:720036"
	922215
	/allele="A"
	/allele="T"
variation	/db_xref="dbSNP:1426389"
	922240
	/allele="C"
	/allele="G"
variation	/db_xref="dbSNP:1426390"
	923190

variation /allele="T"
/allele="C"
/db_xref="dbSNP:1648375"
923206
/allele="G"
/allele="A"
/db_xref="dbSNP:1648376"
variation 923503
/allele="A"
/allele="C"
/db_xref="dbSNP:1426391"
variation 923590
/allele="T"
/allele="G"
/db_xref="dbSNP:1791901"
variation 923789
/allele="G"
/allele="A"
/db_xref="dbSNP:1791900"
variation 924347
/allele="T"
/allele="C"
/db_xref="dbSNP:1791899"
variation 924680
/allele="A"
/allele="G"
/db_xref="dbSNP:1648377"
variation 926588
/allele="T"
/allele="C"
/db_xref="dbSNP:2081579"
variation 926864
/allele="C"
/allele="A"
/db_xref="dbSNP:1612558"
variation 928339
/allele="T"
/allele="A"
/db_xref="dbSNP:1791910"
variation 928660
/allele="T"
/allele="C"
/db_xref="dbSNP:1648364"
variation 928727
/allele="T"
/allele="C"
/db_xref="dbSNP:1648363"
variation 928794
/allele="T"
/allele="C"
/db_xref="dbSNP:1648362"
STS 928957..929084
/standard_name="D11S2331"
/db_xref="UniSTS:51160"
variation 929087
/allele="G"
/allele="A"
/db_xref="dbSNP:1648361"
variation 933504
/allele="C"

```

/allele="T"
/db_xref="dbSNP:1791908"
variation 942201
/allele="G"
/allele="A"
/db_xref="dbSNP:1895915"
variation 942535
/allele="T"
/allele="A"
/db_xref="dbSNP:1648360"
variation 942547
/allele="T"
/allele="G"
/db_xref="dbSNP:2017290"
variation 944081
/allele="G"
/allele="A"
/db_xref="dbSNP:1791914"
STS 951860..952019
/standard_name="C95621"
/db_xref="UniSTS:51531"
variation 952981
/allele="C"
/allele="G"
/db_xref="dbSNP:2033080"
STS 953014..953136
/standard_name="stSG29477"
/db_xref="UniSTS:46076"
STS 953020..953119
/standard_name="SHGC-130661"
/db_xref="UniSTS:137165"
variation 953060
/allele="C"
/allele="T"
/db_xref="dbSNP:1689"
variation 953109
/allele="C"
/allele="T"
/db_xref="dbSNP:1690"
variation 953743
/allele="T"
/allele="G"
/db_xref="dbSNP:1791913"
variation 953774
/allele="G"
/allele="T"
/db_xref="dbSNP:1648365"
variation 954422
/allele="C"
/allele="G"
/db_xref="dbSNP:1426387"
variation 954820
/allele="A"
/allele="G"
/db_xref="dbSNP:1426388"
variation 955233
/allele="T"
/allele="C"
/db_xref="dbSNP:2186419"
variation 958521

```

```

/allele="G"
/allele="T"
/db_xref="dbSNP:2217084"
variation 958566
/allele="C"
/allele="T"
/db_xref="dbSNP:2217085"
variation 959603
/allele="G"
/allele="T"
/db_xref="dbSNP:580025"
variation 960210
/allele="T"
/allele="C"
/db_xref="dbSNP:1557450"
variation 960265
/allele="G"
/allele="A"
/db_xref="dbSNP:1557449"
variation 960567
/allele="T"
/allele="C"
/db_xref="dbSNP:1557448"
variation 960722
/allele="G"
/allele="A"
/db_xref="dbSNP:1648366"
variation 961181
/allele="C"
/allele="T"
/db_xref="dbSNP:523991"
STS 961484..961621
/standard_name="C95586"
/db_xref="UniSTS:51856"
variation 961917
/allele="C"
/allele="T"
/db_xref="dbSNP:516839"
variation 962447
/allele="A"
/allele="G"
/db_xref="dbSNP:491198"
STS 963392..963811
/standard_name="AffySTS000003"
/db_xref="UniSTS:117708"
variation 963499
/allele="G"
/allele="C"
/db_xref="dbSNP:16749"
STS 963589..963782
/standard_name="SHGC-130762"
/db_xref="UniSTS:137244"
variation 965306
/allele="C"
/allele="G"
/db_xref="dbSNP:563942"
variation 965929
/allele="T"
/allele="C"
/db_xref="dbSNP:537328"

```

variation 966359
/allele="C"
/allele="T"
/db_xref="dbSNP:533918"

variation 966455
/allele="C"
/allele="G"
/db_xref="dbSNP:534773"

variation 969847
/allele="A"
/allele="G"
/db_xref="dbSNP:573713"

variation 971730
/allele="A"
/allele="G"
/db_xref="dbSNP:1791890"

variation 974542
/allele="C"
/allele="A"
/db_xref="dbSNP:476007"

STS 974646..974870
/standard_name="C95575"
/db_xref="UniSTS:11867"

variation 975078
/allele="T"
/allele="C"
/db_xref="dbSNP:560009"

variation 976114
/allele="C"
/allele="T"
/db_xref="dbSNP:527557"

variation 976720
/allele="A"
/allele="C"
/db_xref="dbSNP:1783236"

variation 976738
/allele="G"
/allele="T"
/db_xref="dbSNP:484712"

variation 977007
/allele="A"
/allele="G"
/db_xref="dbSNP:556813"

variation 977212
/allele="C"
/allele="T"
/db_xref="dbSNP:489357"

variation 977296
/allele="C"
/allele="T"
/db_xref="dbSNP:490241"

variation 977315
/allele="A"
/allele="C"
/db_xref="dbSNP:2114306"

variation 977512
/allele="C"
/allele="G"
/db_xref="dbSNP:561393"

variation 977764

	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:564079"
	978006
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:2114307"
	978026
	/allele="T"
	/allele="C"
variation	/db_xref="dbSNP:115140"
	978802
	/allele="C"
	/allele="G"
variation	/db_xref="dbSNP:546129"
	979862
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:1894062"
	980044
	/allele="A"
	/allele="C"
variation	/db_xref="dbSNP:1894063"
	980238
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:539227"
	980281
	/allele="A"
	/allele="C"
variation	/db_xref="dbSNP:1240162"
	980371
	/allele="G"
	/allele="C"
variation	/db_xref="dbSNP:513558"
	980922
	/allele="C"
	/allele="A"
variation	/db_xref="dbSNP:1783230"
	981130
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:568523"
	981602
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:573079"
	982877
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:1783229"
	983910
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:518831"
	983937
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:519559"
	985032

	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:573032"
	985042
	/allele="G"
	/allele="T"
variation	/db_xref="dbSNP:1615801"
	985130
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:572075"
	985468
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:548046"
	985517
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:576425"
	987543
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:1648356"
	987886
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:563272"
	988172
	/allele="A"
	/allele="C"
variation	/db_xref="dbSNP:1648357"
	988862
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:483058"
	989235
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:1365322"
	989307
	/allele="C"
	/allele="G"
variation	/db_xref="dbSNP:1365323"
	989363
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:1365324"
	990055
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:1783227"
	990308
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:2033079"
	990483
	/allele="T"
	/allele="C"
variation	/db_xref="dbSNP:1783226"
	990645

	/allele="T"
	/allele="C"
variation	/db_xref="dbSNP:1783225"
	991921
	/allele="A"
	/allele="C"
variation	/db_xref="dbSNP:1240156"
	991927
	/allele="C"
	/allele="G"
variation	/db_xref="dbSNP:1945389"
	992153
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:580777"
	992934
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:518734"
	992998
	/allele="C"
	/allele="A"
variation	/db_xref="dbSNP:1783223"
	993495
	/allele="A"
	/allele="T"
variation	/db_xref="dbSNP:1240157"
	993739
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:1240158"
	993799
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:523193"
	994810
	/allele="T"
	/allele="G"
variation	/db_xref="dbSNP:569587"
	994948
	/allele="C"
	/allele="G"
variation	/db_xref="dbSNP:568552"
	995036
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:1791895"
	995321
	/allele="G"
	/allele="T"
variation	/db_xref="dbSNP:1791898"
	998726
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:504257"
	1000652
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:506373"
	1001073

```

/allele="A"
/allele="C"
/db_xref="dbSNP:510116"
variation 1001823
/allele="A"
/allele="T"
/db_xref="dbSNP:1240152"
variation 1002794
/allele="A"
/allele="G"
/db_xref="dbSNP:1783231"
variation 1003071
/allele="C"
/allele="T"
/db_xref="dbSNP:1791909"
variation 1003077
/allele="A"
/allele="G"
/db_xref="dbSNP:484473"
STS 1009053..1009252
/standard_name="C95574"
/db_xref="UniSTS:64664"
variation 1010847
/allele="A"
/allele="G"
/db_xref="dbSNP:1783219"
variation 1012975
/allele="T"
/allele="C"
/db_xref="dbSNP:1791889"
variation 1013351
/allele="T"
/allele="C"
/db_xref="dbSNP:1627916"
variation 1013837
/allele="T"
/allele="C"
/db_xref="dbSNP:1623650"
variation 1014114
/allele="G"
/allele="A"
/db_xref="dbSNP:1621764"
STS 1015046..1015344
/standard_name="SHGC-140698"
/note="WARNING: map location ambiguous"
/db_xref="UniSTS:140071"
variation 1016095
/allele="C"
/allele="T"
/db_xref="dbSNP:1783220"
variation 1016151
/allele="A"
/allele="G"
/db_xref="dbSNP:1783221"
variation 1016271
/allele="T"
/allele="C"
/db_xref="dbSNP:1618432"
variation 1017043
/allele="A"

```


	/allele="C"
	/db_xref="dbSNP:1619642"
variation	1017071
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:1619708"
variation	1017535
	/allele="C"
	/allele="G"
	/db_xref="dbSNP:1623914"
variation	1017578
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:1624049"
variation	1017797
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:1625804"
variation	1018068
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:1783222"
variation	1018439
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:1791919"
variation	1020614
	/allele="G"
	/allele="C"
	/db_xref="dbSNP:1961328"
variation	1020711
	/allele="T"
	/allele="G"
	/db_xref="dbSNP:1961329"
variation	1021394
	/allele="G"
	/allele="T"
	/db_xref="dbSNP:767102"
variation	1021856
	/allele="G"
	/allele="T"
	/db_xref="dbSNP:1791903"
variation	1022395
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:1783238"
variation	1022463
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:1970737"
variation	1022506
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:1970738"
variation	1022950
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:1791904"
variation	1023198
	/allele="A"

variation /allele="T"
/db_xref="dbSNP:1783232"
1024145
/allele="A"
/allele="C"
/db_xref="dbSNP:1783233"
variation 1024153
/allele="G"
/allele="T"
/db_xref="dbSNP:1791905"
variation 1024348
/allele="C"
/allele="T"
/db_xref="dbSNP:1791906"
variation 1024438
/allele="A"
/allele="G"
/db_xref="dbSNP:1791907"
variation 1025323
/allele="C"
/allele="G"
/db_xref="dbSNP:1783234"
variation 1027812
/allele="A"
/allele="C"
/db_xref="dbSNP:1001061"
variation 1029132
/allele="T"
/allele="C"
/db_xref="dbSNP:1540106"
variation 1030618
/allele="A"
/allele="G"
/db_xref="dbSNP:1783235"
STS 1031536..1031707
/standard_name="C95622"
/db_xref="UniSTS:75518"
variation 1034216
/allele="C"
/allele="T"
/db_xref="dbSNP:882107"
STS 1038688..1038920
/standard_name="C95623"
/db_xref="UniSTS:48242"
variation 1040553
/allele="G"
/allele="T"
/db_xref="dbSNP:1894072"
variation 1040642
/allele="C"
/allele="G"
/db_xref="dbSNP:1894073"
variation 1040777
/allele="C"
/allele="T"
/db_xref="dbSNP:1894074"
variation 1040839
/allele="C"
/allele="G"
/db_xref="dbSNP:1945386"

variation	1051662 /allele="T" /allele="C" /db_xref="dbSNP:1894067"
variation	1052051 /allele="C" /allele="A" /db_xref="dbSNP:1945383"
variation	1052550 /allele="T" /allele="C" /db_xref="dbSNP:1894066"
variation	1054014 /allele="A" /allele="G" /db_xref="dbSNP:1894071"
variation	1057229 /allele="T" /allele="C" /db_xref="dbSNP:1894070"
variation	1057346 /allele="C" /allele="T" /db_xref="dbSNP:874757"
variation	1057410 /allele="T" /allele="C" /db_xref="dbSNP:2156799"
variation	1057609 /allele="G" /allele="A" /db_xref="dbSNP:1894069"
STS	1067347..1067476 /standard_name="D11S4145" /db_xref="UniSTS:49794"
variation	1072326 /allele="A" /allele="T" /db_xref="dbSNP:2007251"
variation	1073933 /allele="A" /allele="G" /db_xref="dbSNP:1945384"
variation	1074081 /allele="A" /allele="T" /db_xref="dbSNP:1348010"
variation	1074264 /allele="C" /allele="T" /db_xref="dbSNP:1348011"
variation	1074438 /allele="A" /allele="G" /db_xref="dbSNP:1440187"
variation	1075267 /allele="G" /allele="T" /db_xref="dbSNP:1945385"
variation	1086493

	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:1992320"
	1086518
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:1992321"
	1086532
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:1992322"
	1086609
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:1992323"
	1089251
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:920447"
	1092272
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:920448"
	1092521
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:920449"
	1093564
	/allele="C"
	/allele="G"
STS	/db_xref="dbSNP:893841"
	1097639..1097737
	/standard_name="D11S3437"
	/db_xref="UniSTS:152678"
variation	1098144
	/allele="C"
	/allele="T"
STS	/db_xref="dbSNP:1550442"
	1098145..1098331
	/standard_name="D11S144"
	/db_xref="UniSTS:148371"
variation	1099007
	/allele="G"
	/allele="T"
variation	/db_xref="dbSNP:1009746"
	1099839
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:1899053"
	1100887
	/allele="A"
	/allele="C"
variation	/db_xref="dbSNP:1440190"
	1100909
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:1440191"
	1102624
	/allele="C"
	/allele="T"

variation /db_xref="dbSNP:1530174"
1102920
/allele="C"
/allele="T"
variation /db_xref="dbSNP:2119193"
1103201
/allele="C"
/allele="T"
variation /db_xref="dbSNP:1550443"
1104682
/allele="C"
/allele="T"
variation /db_xref="dbSNP:920450"
1106636
/allele="C"
/allele="T"
STS /db_xref="dbSNP:2033892"
1109098..1109406
/standard_name="SHGC-105503"
variation /db_xref="UniSTS:136039"
1111512
/allele="A"
/allele="G"
variation /db_xref="dbSNP:1371700"
1111715
/allele="C"
/allele="G"
variation /db_xref="dbSNP:1371701"
1112806
/allele="C"
/allele="G"
variation /db_xref="dbSNP:1992324"
1118062
/allele="C"
/allele="T"
variation /db_xref="dbSNP:1030972"
1118110
/allele="C"
/allele="G"
variation /db_xref="dbSNP:1030973"
1123388
/allele="C"
/allele="T"
variation /db_xref="dbSNP:1017477"
1123472
/allele="A"
/allele="T"
variation /db_xref="dbSNP:1017478"
1126718
/allele="T"
/allele="C"
variation /db_xref="dbSNP:876411"
1126840
/allele="A"
/allele="G"
variation /db_xref="dbSNP:893842"
1128693
/allele="A"
/allele="G"
/db_xref="dbSNP:2053402"

STS 1133312..1133432
/standard_name="C95626"
/db_xref="UniSTS:70841"

variation 1134586
/allele="C"
/allele="T"
/db_xref="dbSNP:1550440"

variation 1134689
/allele="C"
/allele="T"
/db_xref="dbSNP:1550441"

variation 1135652
/allele="C"
/allele="T"
/db_xref="dbSNP:1440192"

variation 1137134
/allele="G"
/allele="T"
/db_xref="dbSNP:1440193"

variation 1139921
/allele="C"
/allele="T"
/db_xref="dbSNP:1371702"

variation 1140011
/allele="C"
/allele="T"
/db_xref="dbSNP:1371703"

variation 1140015
/allele="C"
/allele="T"
/db_xref="dbSNP:2196888"

variation 1140218
/allele="A"
/allele="G"
/db_xref="dbSNP:2165256"

STS 1143525..1143634
/standard_name="SHGC-145350"
/db_xref="UniSTS:174526"

variation 1143684
/allele="T"
/allele="G"
/db_xref="dbSNP:714252"

variation 1144829
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
/db_xref="dbSNP:1354975"

variation 1145013
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:556436"

variation 1145112
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
/db_xref="dbSNP:1354976"

variation 1145112
/note="WARNING: map location ambiguous"
/allele="T"

variation /allele="C"
/db_xref="dbSNP:495033"
1145187
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
/db_xref="dbSNP:1508107"
variation 1145187
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:494200"
variation 1145279
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:493308"
variation 1145492
/note="WARNING: map location ambiguous"
/allele="T"
/allele="G"
/db_xref="dbSNP:491428"
variation 1145596
/note="WARNING: map location ambiguous"
/allele="A"
/allele="T"
/db_xref="dbSNP:490526"
variation 1147771
/allele="G"
/allele="A"
/db_xref="dbSNP:1595831"
variation 1151605
/allele="G"
/allele="A"
/db_xref="dbSNP:1530173"
STS 1153106..1153248
/standard_name="C95591"
/db_xref="UniSTS:46425"
variation 1155411
/allele="G"
/allele="A"
/db_xref="dbSNP:2165255"
variation 1155425
/allele="G"
/allele="C"
/db_xref="dbSNP:2165254"
variation 1157714
/allele="A"
/allele="G"
/db_xref="dbSNP:766722"
variation 1159807
/allele="G"
/allele="C"
/db_xref="dbSNP:1440189"
variation 1159908
/allele="T"
/allele="C"
/db_xref="dbSNP:1440188"
variation 1161602
/allele="T"

	/allele="G"
	/db_xref="dbSNP:766085"
variation	1162486
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:1440194"
variation	1163019
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:920451"
variation	1163073
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:920452"
variation	1163130
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:920453"
variation	1164171
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:2033888"
variation	1164506
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:2033889"
variation	1164528
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:2033890"
variation	1165577
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:1470110"
variation	1165691
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:1470111"
variation	1166230
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:1440195"
variation	1166795
	/allele="A"
	/allele="T"
	/db_xref="dbSNP:920454"
variation	1168196
	/allele="A"
	/allele="C"
	/db_xref="dbSNP:1946897"
variation	1169004
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:930431"
variation	1170968
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:1017479"
variation	1171081
	/allele="A"

variation /allele="G"
/db_xref="dbSNP:1017480"
1171221
/allele="G"
/allele="T"
/db_xref="dbSNP:1017481"
variation 1171748
/allele="C"
/allele="G"
/db_xref="dbSNP:1371704"
variation 1172006
/allele="A"
/allele="T"
/db_xref="dbSNP:986395"
variation 1172083
/allele="C"
/allele="T"
/db_xref="dbSNP:1371693"
variation 1172118
/allele="A"
/allele="G"
/db_xref="dbSNP:1371694"
variation 1172174
/allele="A"
/allele="G"
/db_xref="dbSNP:1371695"
variation 1173723
/allele="A"
/allele="C"
/db_xref="dbSNP:1371696"
variation 1173886
/allele="A"
/allele="G"
/db_xref="dbSNP:1371697"
variation 1174067
/allele="A"
/allele="G"
/db_xref="dbSNP:1371698"
variation 1176528
/allele="C"
/allele="T"
/db_xref="dbSNP:1440181"
variation 1176590
/allele="C"
/allele="T"
/db_xref="dbSNP:1440182"
variation 1178800
/allele="A"
/allele="C"
/db_xref="dbSNP:2033891"
variation 1180556
/allele="A"
/allele="G"
/db_xref="dbSNP:930430"
variation 1180884
/allele="C"
/allele="T"
/db_xref="dbSNP:893837"
variation 1181040
/note="WARNING: map location ambiguous"

	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:893838"
	1181516
	/allele="A"
	/allele="T"
variation	/db_xref="dbSNP:893839"
	1182779
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:893840"
	1185256
	/allele="G"
	/allele="T"
variation	/db_xref="dbSNP:750055"
	1185342
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:750056"
	1185831
	/allele="T"
	/allele="G"
variation	/db_xref="dbSNP:750059"
	1185880
	/allele="G"
	/allele="C"
variation	/db_xref="dbSNP:750058"
	1185881
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:750057"
	1186269
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:1440183"
	1186296
	/allele="A"
	/allele="C"
variation	/db_xref="dbSNP:1440184"
	1186557
	/allele="A"
	/allele="T"
variation	/db_xref="dbSNP:1440185"
	1191442
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:1371699"
	1193524
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:540499"
	1199203
	/allele="G"
	/allele="C"
variation	/db_xref="dbSNP:570448"
	1199484
	/allele="C"
	/allele="A"
variation	/db_xref="dbSNP:567681"
	1199530

	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:558659"
	1199580
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:545657"
	1201697
	/allele="A"
	/allele="C"
variation	/db_xref="dbSNP:693448"
	1201929
	/allele="G"
	/allele="T"
variation	/db_xref="dbSNP:552104"
	1202218
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:569304"
	1202229
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:554865"
	1202834
	/allele="C"
	/allele="G"
variation	/db_xref="dbSNP:560299"
	1202889
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:560476"
	1203341
	/allele="C"
	/allele="G"
variation	/db_xref="dbSNP:490257"
	1203408
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:476367"
	1205149
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:534437"
	1205359
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:551372"
	1205620
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:553449"
	1205942
	/allele="A"
	/allele="C"
variation	/db_xref="dbSNP:556194"
	1206134
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:564591"
	1206176

variation /allele="G"
/allele="T"
/db_xref="dbSNP:579706"
1206274
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
/db_xref="dbSNP:565578"
variation 1206546
/note="WARNING: map location ambiguous"
/allele="A"
/allele="C"
/db_xref="dbSNP:568306"
variation 1207016
/allele="A"
/allele="G"
/db_xref="dbSNP:483448"
variation 1207392
/allele="C"
/allele="T"
/db_xref="dbSNP:501755"
variation 1207735
/allele="C"
/allele="G"
/db_xref="dbSNP:1899052"
variation 1207775
/allele="A"
/allele="G"
/db_xref="dbSNP:505349"
variation 1207882
/allele="C"
/allele="G"
/db_xref="dbSNP:491113"
variation 1209034
/allele="C"
/allele="T"
/db_xref="dbSNP:577853"
variation 1209061
/allele="A"
/allele="G"
/db_xref="dbSNP:577941"
variation 1209433
/allele="C"
/allele="T"
/db_xref="dbSNP:562236"
variation 1209616
/allele="A"
/allele="G"
/db_xref="dbSNP:564046"
variation 1209680
/allele="C"
/allele="T"
/db_xref="dbSNP:472950"
variation 1210030
/allele="A"
/allele="G"
/db_xref="dbSNP:497898"
variation 1210458
/allele="A"
/allele="G"

variation	/db_xref="dbSNP:482795"
	1211470
	/allele="A"
	/allele="C"
variation	/db_xref="dbSNP:531852"
	1212718
	/allele="C"
	/allele="G"
variation	/db_xref="dbSNP:579078"
	1213213
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:1660077"
	1214611
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:513935"
	1216414
	/allele="A"
	/allele="T"
variation	/db_xref="dbSNP:572619"
	1216600
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:478350"
	1216628
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:574529"
	1216803
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:575636"
	1216898
	/allele="C"
	/allele="G"
variation	/db_xref="dbSNP:576510"
	1217776
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:495430"
	1219240
	/allele="A"
	/allele="T"
variation	/db_xref="dbSNP:545675"
	1219243
	/allele="A"
	/allele="C"
variation	/db_xref="dbSNP:545678"
	1219397
	/allele="C"
	/allele="A"
variation	/db_xref="dbSNP:548891"
	1219546
	/allele="T"
	/allele="C"
variation	/db_xref="dbSNP:526151"
	1219788
	/allele="A"
	/allele="G"

variation	/db_xref="dbSNP:571139" 1219874 /allele="A" /allele="C"
variation	/db_xref="dbSNP:572448" 1220553 /allele="C" /allele="T"
variation	/db_xref="dbSNP:488435" 1220596 /allele="A" /allele="G"
variation	/db_xref="dbSNP:1968541" 1220730 /allele="T" /allele="C"
variation	/db_xref="dbSNP:494777" 1220741 /allele="C" /allele="T"
variation	/db_xref="dbSNP:490296" 1220805 /allele="A" /allele="G"
variation	/db_xref="dbSNP:491111" 1221586 /allele="C" /allele="T"
variation	/db_xref="dbSNP:519390" 1222513 /allele="C" /allele="G"
variation	/db_xref="dbSNP:567559" 1223307 /allele="G" /allele="A"
variation	/db_xref="dbSNP:577176" 1223396 /allele="G" /allele="A"
variation	/db_xref="dbSNP:501652" 1224613 /allele="A" /allele="C"
variation	/db_xref="dbSNP:533735" 1227038 /allele="A" /allele="T"
variation	/db_xref="dbSNP:508731" 1228121 /allele="A" /allele="G"
variation	/db_xref="dbSNP:487962" 1229638 /allele="G" /allele="T"
variation	/db_xref="dbSNP:512588" 1230033 /allele="G" /allele="C"

variation	/db_xref="dbSNP:516169" 1230271 /allele="C" /allele="T"
variation	/db_xref="dbSNP:1440186" 1230530 /allele="A" /allele="C"
variation	/db_xref="dbSNP:493693" 1230541 /allele="A" /allele="G"
variation	/db_xref="dbSNP:493721" 1232877 /allele="C" /allele="G"
variation	/db_xref="dbSNP:566174" 1233056 /allele="A" /allele="G"
variation	/db_xref="dbSNP:556727" 1233395 /allele="A" /allele="C"
variation	/db_xref="dbSNP:481473" 1234132 /allele="A" /allele="T"
variation	/db_xref="dbSNP:477364" 1234202 /allele="A" /allele="C"
variation	/db_xref="dbSNP:477546" 1234211 /allele="A" /allele="C"
variation	/db_xref="dbSNP:510206" 1234285 /allele="C" /allele="T"
variation	/db_xref="dbSNP:499794" 1234397 /allele="C" /allele="T"
variation	/db_xref="dbSNP:511919" 1234491 /allele="A" /allele="C"
variation	/db_xref="dbSNP:471763" 1234510 /allele="C" /allele="T"
variation	/db_xref="dbSNP:1790047" 1234562 /allele="A" /allele="T"
variation	/db_xref="dbSNP:502483" 1234784 /allele="G" /allele="T"

variation	/db_xref="dbSNP:504351" 1234886 /allele="C" /allele="T"
variation	/db_xref="dbSNP:516366" 1234893 /allele="C" /allele="G"
variation	/db_xref="dbSNP:516370" 1234977 /allele="A" /allele="C"
variation	/db_xref="dbSNP:517270" 1236271 /allele="C" /allele="T"
variation	/db_xref="dbSNP:571385" 1236615 /allele="A" /allele="G"
variation	/db_xref="dbSNP:574951" 1237524 /allele="G" /allele="T"
variation	/db_xref="dbSNP:516448" 1238080 /allele="C" /allele="T"
variation	/db_xref="dbSNP:521175" 1238229 /allele="G" /allele="T"
variation	/db_xref="dbSNP:543925" 1239485 /allele="G" /allele="A"
variation	/db_xref="dbSNP:548055" 1239556 /allele="A" /allele="T"
variation	/db_xref="dbSNP:513470" 1239838 /allele="A" /allele="G"
variation	/db_xref="dbSNP:516121" 1240155 /allele="T" /allele="C"
variation	/db_xref="dbSNP:542426" 1242892 /allele="A" /allele="T"
variation	/db_xref="dbSNP:496822" 1242903 /allele="A" /allele="C"
variation	/db_xref="dbSNP:496855" 1243576 /allele="A" /allele="G"

variation	/db_xref="dbSNP:1940141" 1244447 /allele="A" /allele="G"
variation	/db_xref="dbSNP:531860" 1244813 /allele="A" /allele="G"
variation	/db_xref="dbSNP:1940142" 1244850 /allele="A" /allele="T"
variation	/db_xref="dbSNP:721189" 1247367 /allele="T" /allele="C"
variation	/db_xref="dbSNP:1940135" 1247840 /allele="A" /allele="G"
variation	/db_xref="dbSNP:537538" 1247878 /allele="T" /allele="C"
variation	/db_xref="dbSNP:555699" 1248293 /allele="T" /allele="C"
variation	/db_xref="dbSNP:552035" 1251439 /allele="T" /allele="A"
variation	/db_xref="dbSNP:512168" 1252761 /allele="C" /allele="G"
variation	/db_xref="dbSNP:2226637" 1252990 /allele="A" /allele="G"
variation	/db_xref="dbSNP:503023" 1253865 /allele="A" /allele="G"
variation	/db_xref="dbSNP:532227" 1253997 /allele="C" /allele="T"
variation	/db_xref="dbSNP:533240" 1255770 /allele="G" /allele="T"
variation	/db_xref="dbSNP:693284" 1256282 /allele="C" /allele="T"
variation	/db_xref="dbSNP:505128" 1256340 /allele="G" /allele="T"

variation	/db_xref="dbSNP:508023" 1256341 /allele="A" /allele="T"
variation	/db_xref="dbSNP:508025" 1258857 /allele="A" /allele="C"
variation	/db_xref="dbSNP:573126" 1259850 /allele="T" /allele="C"
variation	/db_xref="dbSNP:1940143" 1260418 /allele="G" /allele="C"
variation	/db_xref="dbSNP:519971" 1260436 /allele="A" /allele="G"
variation	/db_xref="dbSNP:553344" 1261583 /allele="C" /allele="T"
variation	/db_xref="dbSNP:575623" 1262063 /allele="C" /allele="T"
variation	/db_xref="dbSNP:579941" 1262198 /allele="C" /allele="T"
variation	/db_xref="dbSNP:580965" 1263023 /allele="A" /allele="C"
variation	/db_xref="dbSNP:508994" 1263459 /allele="A" /allele="T"
variation	/db_xref="dbSNP:533848" 1263736 /allele="C" /allele="G"
variation	/db_xref="dbSNP:536484" 1263940 /allele="C" /allele="T"
variation	/db_xref="dbSNP:538359" 1266921 /allele="G" /allele="T"
variation	/db_xref="dbSNP:509101" 1268309 /allele="A" /allele="G"
variation	/db_xref="dbSNP:563990" 1268701 /allele="A" /allele="G"

STS	/db_xref="dbSNP:576670"
	1269990..1270310
	/standard_name="SHGC-143237"
	/db_xref="UniSTS:171832"
variation	1270108
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:534082"
variation	1270957
	/allele="C"
	/allele="G"
	/db_xref="dbSNP:563229"
variation	1271329
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:578780"
variation	1274478
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:544154"
variation	1275034
	/allele="A"
	/allele="C"
	/db_xref="dbSNP:574778"
variation	1275096
	/allele="C"
	/allele="G"
	/db_xref="dbSNP:571506"
variation	1275294
	/allele="C"
	/allele="G"
	/db_xref="dbSNP:487457"
variation	1275385
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:571025"
variation	1275447
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:489212"
variation	1275899
	/allele="C"
	/allele="A"
	/db_xref="dbSNP:506972"
variation	1276136
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:505009"
variation	1276510
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:501433"
variation	1277405
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:471840"
variation	1277435
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:471750"

<u>variation</u>	1278529 /allele="G" /allele="T" /db_xref="dbSNP:574233"
<u>variation</u>	1279014 /allele="G" /allele="A" /db_xref="dbSNP:693603"
<u>variation</u>	1280168 /allele="T" /allele="C" /db_xref="dbSNP:483367"
<u>variation</u>	1281138 /allele="C" /allele="A" /db_xref="dbSNP:490592"
<u>variation</u>	1281419 /allele="G" /allele="A" /db_xref="dbSNP:561496"
<u>variation</u>	1285306 /allele="C" /allele="A" /db_xref="dbSNP:477952"
<u>variation</u>	1285324 /allele="T" /allele="C" /db_xref="dbSNP:565706"
<u>variation</u>	1285367 /allele="T" /allele="C" /db_xref="dbSNP:477148"
<u>variation</u>	1285706 /allele="C" /allele="A" /db_xref="dbSNP:474230"
<u>variation</u>	1286265 /allele="T" /allele="A" /db_xref="dbSNP:558243"
<u>variation</u>	1287754 /allele="G" /allele="A" /db_xref="dbSNP:2174880"
<u>variation</u>	1289379 /allele="T" /allele="C" /db_xref="dbSNP:2135994"
<u>variation</u>	1289443 /allele="T" /allele="C" /db_xref="dbSNP:2135993"
<u>variation</u>	1289503 /allele="T" /allele="C" /db_xref="dbSNP:2135992"
<u>variation</u>	1289625 /allele="T" /allele="C" /db_xref="dbSNP:2174879"

variation	1291774 /allele="G" /allele="C" /db_xref="dbSNP:472726"
variation	1293629 /allele="G" /allele="A" /db_xref="dbSNP:580872"
variation	1293671 /allele="T" /allele="A" /db_xref="dbSNP:580779"
variation	1293957 /allele="G" /allele="C" /db_xref="dbSNP:1508105"
variation	1293981 /allele="G" /allele="A" /db_xref="dbSNP:534845"
variation	1294279 /allele="G" /allele="A" /db_xref="dbSNP:532107"
variation	1294548 /allele="T" /allele="C" /db_xref="dbSNP:529411"
variation	1295414 /allele="T" /allele="C" /db_xref="dbSNP:500943"
variation	1295625 /allele="G" /allele="A" /db_xref="dbSNP:1508104"
variation	1295643 /allele="G" /allele="A" /db_xref="dbSNP:548890"
variation	1295697 /allele="G" /allele="C" /db_xref="dbSNP:486476"
variation	1295729 /allele="G" /allele="A" /db_xref="dbSNP:485778"
variation	1296524 /allele="T" /allele="C" /db_xref="dbSNP:541407"
variation	1297637 /allele="C" /allele="A" /db_xref="dbSNP:565622"
variation	1297731 /allele="T" /allele="C" /db_xref="dbSNP:547761"

variation	1298335 /allele="G" /allele="T" /db_xref="dbSNP:2221632"
variation	1298514 /allele="A" /allele="G" /db_xref="dbSNP:575549"
variation	1298944 /allele="A" /allele="G" /db_xref="dbSNP:490043"
variation	1299548 /allele="C" /allele="T" /db_xref="dbSNP:489164"
variation	1299584 /allele="A" /allele="G" /db_xref="dbSNP:505390"
variation	1299734 /allele="A" /allele="G" /db_xref="dbSNP:504339"
variation	1300170 /allele="C" /allele="T" /db_xref="dbSNP:1911698"
variation	1301992 /allele="C" /allele="T" /db_xref="dbSNP:505064"
variation	1302013 /allele="G" /allele="T" /db_xref="dbSNP:505123"
variation	1303454 /allele="A" /allele="G" /db_xref="dbSNP:489303"
variation	1303710 /allele="A" /allele="G" /db_xref="dbSNP:512352"
variation	1304082 /allele="T" /allele="C" /db_xref="dbSNP:503361"
variation	1304330 /allele="A" /allele="T" /db_xref="dbSNP:517821"
variation	1304398 /allele="T" /allele="C" /db_xref="dbSNP:500613"
variation	1304751 /allele="G" /allele="A" /db_xref="dbSNP:573052"

variation 1305590
/allele="C"
/allele="T"
/db_xref="dbSNP:550791"
variation 1305772
/allele="G"
/allele="A"
/db_xref="dbSNP:542671"
variation 1305919
/allele="T"
/allele="C"
/db_xref="dbSNP:541643"
variation 1307927
/allele="G"
/allele="C"
/db_xref="dbSNP:580363"
variation 1308117
/allele="T"
/allele="A"
/db_xref="dbSNP:492509"
variation 1308213
/allele="T"
/allele="G"
/db_xref="dbSNP:491575"
misc_feature 1308367..2453337
/standard_name="RP11-356E17"
/note="FISH-mapped clone"
/map="11q23.2c-11q23.3a (NCI) "
variation 1308761
/allele="T"
/allele="C"
/db_xref="dbSNP:552043"
variation 1309457
/allele="G"
/allele="A"
/db_xref="dbSNP:522098"
variation 1311433
/allele="T"
/allele="G"
/db_xref="dbSNP:574449"
variation 1311493
/allele="T"
/allele="G"
/db_xref="dbSNP:1616236"
variation 1311505
/allele="T"
/allele="A"
/db_xref="dbSNP:571831"
variation 1311801
/allele="T"
/allele="G"
/db_xref="dbSNP:574223"
variation 1311848
/allele="G"
/allele="A"
/db_xref="dbSNP:570745"
variation 1311897
/allele="T"
/allele="C"
/db_xref="dbSNP:547021"

variation	1311943 /allele="T" /allele="C" /db_xref="dbSNP:517599"
variation	1312508 /allele="G" /allele="A" /db_xref="dbSNP:541563"
variation	1312675 /allele="C" /allele="A" /db_xref="dbSNP:518684"
variation	1313368 /allele="G" /allele="A" /db_xref="dbSNP:514112"
variation	1313490 /allele="T" /allele="C" /db_xref="dbSNP:513083"
variation	1313747 /allele="G" /allele="C" /db_xref="dbSNP:487611"
variation	1314715 /allele="T" /allele="C" /db_xref="dbSNP:568466"
variation	1314718 /allele="C" /allele="A" /db_xref="dbSNP:560801"
variation	1316182 /allele="A" /allele="C" /db_xref="dbSNP:1789405"
variation	1316615 /allele="A" /allele="C" /db_xref="dbSNP:1789406"
variation	1318515 /allele="C" /allele="A" /db_xref="dbSNP:1631183"
variation	1319449 /allele="G" /allele="C" /db_xref="dbSNP:1508101"
variation	1319907 /allele="G" /allele="C" /db_xref="dbSNP:1508100"
variation	1321285 /allele="C" /allele="A" /db_xref="dbSNP:1508099"
variation	1321670 /allele="G" /allele="A" /db_xref="dbSNP:1508098"

variation 1323896
/allele="T"
/allele="A"
/db_xref="dbSNP:1848373"

variation 1323926
/allele="G"
/allele="C"
/db_xref="dbSNP:491076"

variation 1324038
/allele="T"
/allele="C"
/db_xref="dbSNP:490145"

variation 1324546
/allele="T"
/allele="C"
/db_xref="dbSNP:1960358"

variation 1324724
/allele="T"
/allele="G"
/db_xref="dbSNP:963417"

variation 1327502
/allele="C"
/allele="A"
/db_xref="dbSNP:505294"

variation 1330929
/allele="G"
/allele="A"
/db_xref="dbSNP:2102405"

variation 1331582
/allele="T"
/allele="C"
/db_xref="dbSNP:884496"

variation 1331610
/allele="T"
/allele="C"
/db_xref="dbSNP:906543"

variation 1335098
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
/db_xref="dbSNP:1354975"

variation 1335282
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:556436"

variation 1335381
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
/db_xref="dbSNP:1354976"

variation 1335381
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:495033"

variation 1335456
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"

variation /db_xref="dbSNP:1508107"
1335456
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
variation /db_xref="dbSNP:494200"
1335548
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
variation /db_xref="dbSNP:493308"
1335761
/note="WARNING: map location ambiguous"
/allele="T"
/allele="G"
variation /db_xref="dbSNP:491428"
1335865
/note="WARNING: map location ambiguous"
/allele="A"
/allele="T"
variation /db_xref="dbSNP:490526"
1336857
/allele="C"
/allele="T"
variation /db_xref="dbSNP:1828119"
1336943
/allele="A"
/allele="C"
variation /db_xref="dbSNP:1702863"
1336962
/allele="C"
/allele="T"
variation /db_xref="dbSNP:1828120"
1336970
/allele="A"
/allele="G"
variation /db_xref="dbSNP:1828121"
1337225
/allele="G"
/allele="A"
variation /db_xref="dbSNP:549298"
1338437
/allele="A"
/allele="G"
variation /db_xref="dbSNP:693192"
1338619
/allele="C"
/allele="T"
variation /db_xref="dbSNP:573554"
1338984
/allele="C"
/allele="T"
variation /db_xref="dbSNP:1158260"
1339479
/allele="A"
/allele="G"
variation /db_xref="dbSNP:1508108"
1343703
/allele="G"
/allele="A"

```

variation      /db_xref="dbSNP:2063175"
                1345993
                /allele="T"
                /allele="C"
variation      /db_xref="dbSNP:2135991"
                1346234
                /allele="T"
                /allele="C"
variation      /db_xref="dbSNP:2174878"
                1350958
                /allele="G"
                /allele="A"
variation      /db_xref="dbSNP:1508106"
                1350986
                /allele="T"
                /allele="A"
variation      /db_xref="dbSNP:1396132"
                1351206
                /allele="C"
                /allele="A"
variation      /db_xref="dbSNP:1396131"
                1352360
                /allele="A"
                /allele="C"
variation      /db_xref="dbSNP:1944156"
                1356623
                /allele="A"
                /allele="C"
STS            /db_xref="dbSNP:2187394"
                1363555..1363864
                /standard_name="SHGC-148312"
                /db_xref="UniSTS:176315"
variation      1363843
                /allele="G"
                /allele="A"
variation      /db_xref="dbSNP:884386"
                1364070
                /allele="G"
                /allele="A"
variation      /db_xref="dbSNP:868066"
                1365540
                /allele="C"
                /allele="A"
variation      /db_xref="dbSNP:951839"
                1369440
                /allele="G"
                /allele="T"
variation      /db_xref="dbSNP:925152"
                1377411
                /allele="C"
                /allele="T"
STS            /db_xref="dbSNP:884603"
                1377524..1377840
                /standard_name="SHGC-148838"
                /db_xref="UniSTS:176636"
variation      1381849
                /allele="C"
                /allele="T"
variation      /db_xref="dbSNP:1962593"
                1382638

```

```

/allele="A"
/allele="G"
/db_xref="dbSNP:906542"
variation 1384259
/allele="C"
/allele="G"
/db_xref="dbSNP:2063176"
variation 1388382
/allele="C"
/allele="T"
/db_xref="dbSNP:2174877"
variation 1392767
/allele="A"
/allele="G"
/db_xref="dbSNP:1828118"
variation 1395435
/allele="A"
/allele="G"
/db_xref="dbSNP:2174876"
variation 1395964
/allele="C"
/allele="T"
/db_xref="dbSNP:906539"
variation 1396190
/allele="A"
/allele="T"
/db_xref="dbSNP:906540"
variation 1396272
/allele="A"
/allele="G"
/db_xref="dbSNP:906541"
variation 1406291
/allele="A"
/allele="G"
/db_xref="dbSNP:925151"
variation 1407100
/allele="C"
/allele="T"
/db_xref="dbSNP:1108627"
variation 1407991
/allele="T"
/allele="G"
/db_xref="dbSNP:881517"
variation 1408609
/allele="C"
/allele="G"
/db_xref="dbSNP:906545"
STS 1410841..1411122
/standard_name="SHGC-156298"
/db_xref="UniSTS:182475"
variation 1410918
/allele="C"
/allele="T"
/db_xref="dbSNP:883283"
variation 1411661
/allele="G"
/allele="A"
/db_xref="dbSNP:906546"
variation 1411744
/allele="C"

```

variation /allele="T"
/db_xref="dbSNP:883863"
1412447
/allele="T"
/allele="C"
variation /db_xref="dbSNP:867899"
1412455
/allele="G"
/allele="A"
variation /db_xref="dbSNP:867898"
1412497
/allele="G"
/allele="C"
variation /db_xref="dbSNP:867897"
1415414
/allele="G"
/allele="A"
variation /db_xref="dbSNP:2135990"
1416635
/allele="G"
/allele="A"
variation /db_xref="dbSNP:1039755"
1420783
/allele="T"
/allele="C"
variation /db_xref="dbSNP:1508103"
1420872
/allele="T"
/allele="C"
STS /db_xref="dbSNP:1508102"
1421813..1422157
/standard_name="SHGC-83395"
variation /db_xref="UniSTS:101901"
1426362
/allele="G"
/allele="A"
variation /db_xref="dbSNP:906544"
1427310
/allele="A"
/allele="G"
variation /db_xref="dbSNP:875025"
1427827
/allele="G"
/allele="A"
variation /db_xref="dbSNP:1354974"
1428186
/allele="T"
/allele="C"
variation /db_xref="dbSNP:2003013"
1428347
/allele="T"
/allele="C"
variation /db_xref="dbSNP:879412"
1428558
/allele="T"
/allele="G"
variation /db_xref="dbSNP:879411"
1429202
/note="WARNING: map location ambiguous"
/allele="A"

```
variation    /allele="G"
              /db_xref="dbSNP:180339"
              1430582
              /note="WARNING: map location ambiguous"
              /allele="A"
              /allele="G"
              /db_xref="dbSNP:180340"
variation    1432021
              /note="WARNING: map location ambiguous"
              /allele="C"
              /allele="T"
              /db_xref="dbSNP:180341"
variation    1432037
              /note="WARNING: map location ambiguous"
              /allele="C"
              /allele="T"
              /db_xref="dbSNP:180342"
variation    1432070
              /note="WARNING: map location ambiguous"
              /allele="C"
              /allele="T"
              /db_xref="dbSNP:180343"
variation    1433796
              /note="WARNING: map location ambiguous"
              /allele="A"
              /allele="G"
              /db_xref="dbSNP:180344"
variation    1433963
              /note="WARNING: map location ambiguous"
              /allele="C"
              /allele="T"
              /db_xref="dbSNP:180345"
variation    1434321
              /note="WARNING: map location ambiguous"
              /allele="G"
              /allele="T"
              /db_xref="dbSNP:180346"
variation    1434672
              /note="WARNING: map location ambiguous"
              /allele="C"
              /allele="G"
              /db_xref="dbSNP:180347"
variation    1434989
              /note="WARNING: map location ambiguous"
              /allele="C"
              /allele="T"
              /db_xref="dbSNP:180348"
variation    1435157
              /note="WARNING: map location ambiguous"
              /allele="A"
              /allele="T"
              /db_xref="dbSNP:180349"
variation    1436244
              /note="WARNING: map location ambiguous"
              /allele="C"
              /allele="T"
              /db_xref="dbSNP:1263055"
variation    1436425
              /note="WARNING: map location ambiguous"
              /allele="G"
```

variation /allele="T"
/db_xref="dbSNP:1794200"
1436506
/note="WARNING: map location ambiguous"
/allele="A"
/allele="C"
/db_xref="dbSNP:1794201"
variation 1436510
/note="WARNING: map location ambiguous"
/allele="G"
/allele="C"
/db_xref="dbSNP:1787722"
variation 1436558
/note="WARNING: map location ambiguous"
/allele="A"
/allele="C"
/db_xref="dbSNP:1794202"
variation 1436872
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
/db_xref="dbSNP:1263056"
variation 1437536
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
/db_xref="dbSNP:1263057"
variation 1437736
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:1263058"
variation 1452891
/allele="C"
/allele="A"
/db_xref="dbSNP:2127905"
variation 1455917
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
/db_xref="dbSNP:558229"
variation 1456222
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
/db_xref="dbSNP:573442"
variation 1456342
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
/db_xref="dbSNP:1243244"
variation 1456342
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
/db_xref="dbSNP:473210"
variation 1456401
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"

variation /db_xref="dbSNP:574603"
1456539
/note="WARNING: map location ambiguous"
/allele="T"
/allele="G"

variation /db_xref="dbSNP:687740"
1456609
/note="WARNING: map location ambiguous"
/allele="G"
/allele="T"

variation /db_xref="dbSNP:520909"
1458834
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"

variation /db_xref="dbSNP:610775"
1459354
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"

variation /db_xref="dbSNP:679022"
1462411
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"

variation /db_xref="dbSNP:667944"
1463010
/note="WARNING: map location ambiguous"
/allele="G"
/allele="T"

variation /db_xref="dbSNP:621361"
1463111
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"

variation /db_xref="dbSNP:1261766"
1463111
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"

variation /db_xref="dbSNP:621858"
1463605
/note="WARNING: map location ambiguous"
/allele="T"
/allele="G"

variation /db_xref="dbSNP:534381"
1463653
/note="WARNING: map location ambiguous"
/allele="G"
/allele="T"

variation /db_xref="dbSNP:549936"
1463656
/note="WARNING: map location ambiguous"
/allele="G"
/allele="T"

variation /db_xref="dbSNP:549937"
1463736
/note="WARNING: map location ambiguous"
/allele="G"
/allele="T"

variation /db_xref="dbSNP:1271832"
1463757
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
variation /db_xref="dbSNP:1242885"
1463777
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
variation /db_xref="dbSNP:1242598"
1463782
/note="WARNING: map location ambiguous"
/allele="G"
/allele="T"
variation /db_xref="dbSNP:1263531"
1465199
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
variation /db_xref="dbSNP:1272992"
1465199
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
variation /db_xref="dbSNP:1272994"
1465276
/note="WARNING: map location ambiguous"
/allele="T"
/allele="G"
variation /db_xref="dbSNP:1271274"
1465971
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
variation /db_xref="dbSNP:654926"
1468495
/note="WARNING: map location ambiguous"
/allele="T"
/allele="G"
variation /db_xref="dbSNP:537091"
1468741
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
variation /db_xref="dbSNP:1242697"
1468932
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
variation /db_xref="dbSNP:1242594"
1469397
/note="WARNING: map location ambiguous"
/allele="C"
/allele="G"
variation /db_xref="dbSNP:1242595"
1469940
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"

variation /db_xref="dbSNP:568787"
1470242
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
variation /db_xref="dbSNP:1261744"
1472282
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
variation /db_xref="dbSNP:552803"
1473827
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
STS /db_xref="dbSNP:621188"
1474954..1475164
/standard_name="D11S2829"
/note="WARNING: map location ambiguous"
variation /db_xref="UniSTS:152017"
1475074
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
variation /db_xref="dbSNP:671553"
1476787
/note="WARNING: map location ambiguous"
/allele="T"
/allele="G"
variation /db_xref="dbSNP:684669"
1480474
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
variation /db_xref="dbSNP:521187"
1481835
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
variation /db_xref="dbSNP:679223"
1482007
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
variation /db_xref="dbSNP:506836"
1483426
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
variation /db_xref="dbSNP:634867"
1484123
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
variation /db_xref="dbSNP:648740"
1484465
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:505824"

variation 1484551
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
/db_xref="dbSNP:504935"

variation 1486228
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:557396"

variation 1487453
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:2155394"

variation 1488050
/note="WARNING: map location ambiguous"
/allele="C"
/allele="G"
/db_xref="dbSNP:603858"

variation 1488083
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:499829"

variation 1490388
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:634606"

variation 1490587
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:523825"

variation 1493346
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:1268872"

variation 1493441
/note="WARNING: map location ambiguous"
/allele="C"
/allele="A"
/db_xref="dbSNP:541953"

variation 1493573
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:472785"

variation 1493578
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:540922"

variation 1494467
/note="WARNING: map location ambiguous"
/allele="C"
/allele="A"
/db_xref="dbSNP:511635"

variation 1494481
/note="WARNING: map location ambiguous"
/allele="C"
/allele="A"
/db_xref="dbSNP:651438"

variation 1494503
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:582331"

variation 1494666
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:1243310"

variation 1494824
/note="WARNING: map location ambiguous"
/allele="C"
/allele="A"
/db_xref="dbSNP:639320"

variation 1495119
/allele="G"
/allele="A"
/db_xref="dbSNP:1243309"

variation 1495313
/allele="T"
/allele="C"
/db_xref="dbSNP:1243308"

variation 1495531
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:529470"

variation 1495557
/note="WARNING: map location ambiguous"
/allele="C"
/allele="A"
/db_xref="dbSNP:529408"

variation 1495593
/note="WARNING: map location ambiguous"
/allele="G"
/allele="C"
/db_xref="dbSNP:636076"

variation 1495594
/note="WARNING: map location ambiguous"
/allele="C"
/allele="A"
/db_xref="dbSNP:480200"

variation 1495856
/allele="G"
/allele="A"
/db_xref="dbSNP:1272510"

variation 1495871
/allele="G"
/allele="A"
/db_xref="dbSNP:1243307"

variation 1495898
/allele="T"
/allele="C"
/db_xref="dbSNP:1271860"

variation 1496847
/allele="G"
/allele="A"
/db_xref="dbSNP:1242666"

variation 1497465
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:654926"

variation 1498497
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
/db_xref="dbSNP:477036"

variation 1499049
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
/db_xref="dbSNP:557985"

variation 1501649
/note="WARNING: map location ambiguous"
/allele="C"
/allele="A"
/db_xref="dbSNP:1144037"

variation 1511101
/allele="G"
/allele="T"
/db_xref="dbSNP:569095"

STS 1517955..1518105
/standard_name="SGC34966"
/db_xref="UniSTS:72496"

STS 1518093..1518246
/standard_name="H68114"
/db_xref="UniSTS:19356"

variation 1520150
/allele="T"
/allele="G"
/db_xref="dbSNP:672251"

variation 1521476
/allele="T"
/allele="C"
/db_xref="dbSNP:2155130"

variation 1522236
/allele="T"
/allele="C"
/db_xref="dbSNP:495258"

variation 1523747
/allele="G"
/allele="A"
/db_xref="dbSNP:695083"

variation 1524053
/allele="G"
/allele="A"
/db_xref="dbSNP:1243735"

variation 1524446
/allele="G"
/allele="A"
/db_xref="dbSNP:1270810"

variation 1526137
/allele="G"

variation /allele="A"
/db_xref="dbSNP:512017"
1526301
/allele="G"
/allele="C"
/db_xref="dbSNP:657882"
variation 1527181
/allele="T"
/allele="C"
/db_xref="dbSNP:480801"
variation 1527504
/allele="G"
/allele="A"
/db_xref="dbSNP:613244"
STS 1530483..1530623
/standard_name="D11S3005"
/db_xref="UniSTS:152112"
variation 1532383
/allele="A"
/allele="T"
/db_xref="dbSNP:1893043"
variation 1532393
/allele="A"
/allele="C"
/db_xref="dbSNP:1893044"
variation 1535311
/allele="A"
/allele="G"
/db_xref="dbSNP:632971"
STS 1536465..1536722
/standard_name="D11S1163"
/db_xref="UniSTS:33352"
variation 1537667
/allele="C"
/allele="G"
/db_xref="dbSNP:527005"
STS 1539152..1539314
/standard_name="D11S490"
/db_xref="UniSTS:23790"
STS 1539198..1539353
/standard_name="D11S29"
/db_xref="UniSTS:91102"
variation 1540359
/allele="C"
/allele="T"
/db_xref="dbSNP:666094"
variation 1540393
/allele="G"
/allele="T"
/db_xref="dbSNP:666137"
variation 1540483
/allele="T"
/allele="C"
/db_xref="dbSNP:685184"
variation 1540518
/allele="T"
/allele="G"
/db_xref="dbSNP:685145"
variation 1540779
/allele="G"

```

/allele="C"
/db_xref="dbSNP:683842"
STS 1554872..1555097
/standard_name="FB5D4"
/db_xref="UniSTS:55992"
STS 1562512..1562737
/standard_name="D11S2444"
/note="WARNING: map location ambiguous"
/db_xref="UniSTS:34163"
STS 1565721..1566057
/standard_name="GDB:315997"
/note="WARNING: map location ambiguous"
/db_xref="UniSTS:156559"
STS 1569888..1570113
/standard_name="D11S2444"
/note="WARNING: map location ambiguous"
/db_xref="UniSTS:34163"
variation 1581083
/allele="C"
/allele="G"
/db_xref="dbSNP:722066"
variation 1581137
/allele="G"
/allele="C"
/db_xref="dbSNP:722067"
STS 1581383..1581697
/standard_name="SHGC-106726"
/db_xref="UniSTS:136280"
STS 1581542..1581657
/standard_name="D11S3416"
/db_xref="UniSTS:152657"
variation 1585059
/allele="T"
/allele="G"
/db_xref="dbSNP:2187639"
variation 1595130
/allele="A"
/allele="C"
/db_xref="dbSNP:530943"
STS 1596528..1596775
/standard_name="D11S939"
/note="WARNING: map location ambiguous"
/db_xref="UniSTS:65298"
STS 1596542..1596773
/standard_name="AFM267yh5"
/note="WARNING: map location ambiguous"
/db_xref="UniSTS:16970"
variation 1598174
/allele="A"
/allele="G"
/db_xref="dbSNP:550388"
variation 1598961
/allele="A"
/allele="C"
/db_xref="dbSNP:543057"
variation 1600217
/allele="A"
/allele="C"
/db_xref="dbSNP:489136"
variation 1600276
```

```

variation    /allele="C"
              /allele="T"
              /db_xref="dbSNP:488976"
              1601193
              /allele="G"
              /allele="A"
              /db_xref="dbSNP:565745"
variation    1602197
              /allele="T"
              /allele="G"
              /db_xref="dbSNP:2000562"
variation    1602254
              /allele="T"
              /allele="G"
              /db_xref="dbSNP:2000561"
gene         1602988..1631740
              /gene="MSP"
              /db_xref="LocusID:84000"
mRNA         join(1602988..1603098,1613547..1613976,1615111..1615215,
              1617871..1617990,1618475..1618608,1620525..1620617,
              1621635..1621678,1622417..1622579,1623601..1624590)
              /gene="MSP"
              /product="mosaic serine protease"
              /note="Derived by automated computational analysis.
              Supporting evidence includes similarity to: 1 mRNA"
              /transcript_id="XM_052098.1"
              /db_xref="GI:14774255"
              /db_xref="LocusID:84000"
mRNA         join(1603004..1603098,1613547..1613976,1617871..1617990,
              1618475..1618608,1620525..1620617,1621635..1621678,
              1622417..1622579,1623601..1623773,1626649..1626747,
              1628284..1628426,1628578..1628730,1630120..1631740)
              /gene="MSP"
              /product="mosaic serine protease"
              /note="Derived by automated computational analysis.
              Supporting evidence includes similarity to: 2 mRNAs"
              /transcript_id="XM_052099.1"
              /db_xref="GI:14774251"
              /db_xref="LocusID:84000"
mRNA         join(1603004..1603098,1613547..1613976,1615111..1615215,
              1617871..1617990,1618475..1618608,1620525..1620617,
              1621635..1621678,1622417..1622579,1623601..1623773,
              1626649..1626747,1628284..1628426,1628578..1629340)
              /gene="MSP"
              /product="mosaic serine protease"
              /note="Derived by automated computational analysis.
              Supporting evidence includes similarity to: 1 mRNA"
              /transcript_id="XM_052100.1"
              /db_xref="GI:14774259"
              /db_xref="LocusID:84000"
CDS          join(1603078..1603098,1613547..1613976,1615111..1615215,
              1617871..1617990,1618475..1618488)
              /gene="MSP"
              /codon_start=1
              /protein_id="XP_052098.1"
              /db_xref="GI:14774256"
              /db_xref="LocusID:84000"
variation    1603296
              /gene="MSP"
              /allele="A"

```


variation /allele="G"
/db_xref="dbSNP:722729"
1621482
/gene="MSP"
/allele="T"
/allele="C"
/db_xref="dbSNP:2155195"
variation 1621665
/gene="MSP"
/allele="T"
/allele="C"
/db_xref="dbSNP:2155194"
CDS join(1622434..1622579,1623601..1623773,1626649..1626747,
1628284..1628426,1628578..1628730,1630120..1630146)
/gene="MSP"
/codon_start=1
/protein_id="XP_052099.1"
/db_xref="GI:14774252"
/db_xref="LocusID:84000"
CDS join(1622434..1622579,1623601..1623773,1626649..1626747,
1628284..1628426,1628578..1628814)
/gene="MSP"
/codon_start=1
/protein_id="XP_052100.1"
/db_xref="GI:14774260"
/db_xref="LocusID:84000"
variation 1623488
/gene="MSP"
/allele="T"
/allele="C"
/db_xref="dbSNP:947969"
STS 1624310..1624449
/gene="MSP"
/standard_name="stSG48478"
/db_xref="UniSTS:87232"
variation 1627755
/gene="MSP"
/allele="T"
/allele="C"
/db_xref="dbSNP:1271170"
variation 1628044
/gene="MSP"
/allele="T"
/allele="C"
/db_xref="dbSNP:477408"
variation 1628066
/gene="MSP"
/allele="G"
/allele="A"
/db_xref="dbSNP:686992"
variation 1628954
/gene="MSP"
/allele="G"
/allele="C"
/db_xref="dbSNP:2186627"
variation 1629563
/gene="MSP"
/allele="T"
/allele="C"
/db_xref="dbSNP:947917"

variation 1629990
/gene="MSP"
/allele="C"
/allele="G"
/db_xref="dbSNP:494457"

variation 1630252
/gene="MSP"
/allele="G"
/allele="A"
/db_xref="dbSNP:491822"

variation 1630871
/gene="MSP"
/allele="G"
/allele="C"
/db_xref="dbSNP:575535"

variation 1631212
/gene="MSP"
/allele="G"
/allele="T"
/db_xref="dbSNP:572675"

STS 1631602..1631722
/gene="MSP"
/standard_name="H45485"
/db_xref="UniSTS:72385"

variation 1631703
/gene="MSP"
/allele="G"
/allele="C"
/db_xref="dbSNP:568060"

variation 1632031
/allele="G"
/allele="A"
/db_xref="dbSNP:543480"

variation 1632102
/allele="T"
/allele="G"
/db_xref="dbSNP:543290"

variation 1632325
/allele="A"
/allele="G"
/db_xref="dbSNP:997956"

STS 1632444..1632717
/standard_name="SHGC-140144"
/db_xref="UniSTS:139616"

variation 1632595
/allele="T"
/allele="C"
/db_xref="dbSNP:640483"

variation 1634646
/allele="G"
/allele="A"
/db_xref="dbSNP:755538"

variation 1634691
/allele="T"
/allele="C"
/db_xref="dbSNP:755537"

variation 1635602
/allele="T"
/allele="C"
/db_xref="dbSNP:558247"

variation 1639222
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:1270819"

variation 1639232
/note="WARNING: map location ambiguous"
/allele="T"
/allele="G"
/db_xref="dbSNP:1244228"

variation 1641700
/allele="T"
/allele="G"
/db_xref="dbSNP:1939367"

variation 1641701
/allele="T"
/allele="G"
/db_xref="dbSNP:1939366"

variation 1643032
/allele="G"
/allele="A"
/db_xref="dbSNP:498645"

variation 1644442
/allele="C"
/allele="G"
/db_xref="dbSNP:580287"

variation 1644478
/allele="A"
/allele="C"
/db_xref="dbSNP:580205"

variation 1645755
/allele="C"
/allele="A"
/db_xref="dbSNP:601122"

variation 1646199
/allele="T"
/allele="C"
/db_xref="dbSNP:488827"

variation 1648018
/allele="G"
/allele="A"
/db_xref="dbSNP:1145224"

variation 1648367
/allele="T"
/allele="A"
/db_xref="dbSNP:649670"

variation 1648709
/allele="T"
/allele="C"
/db_xref="dbSNP:534075"

variation 1650645
/allele="A"
/allele="C"
/db_xref="dbSNP:680641"

variation 1650943
/allele="C"
/allele="T"
/db_xref="dbSNP:504672"

variation 1651106
/allele="A"

	/allele="C"
	/db_xref="dbSNP:584994"
variation	1652207
	/allele="G"
	/allele="T"
	/db_xref="dbSNP:2186665"
variation	1652360
	/allele="G"
	/allele="C"
	/db_xref="dbSNP:497768"
variation	1652650
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:602486"
variation	1654622
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:631898"
variation	1656968
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:535190"
variation	1657225
	/allele="C"
	/allele="G"
	/db_xref="dbSNP:537208"
variation	1657441
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:543312"
variation	1657612
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:540850"
variation	1657682
	/allele="A"
	/allele="C"
	/db_xref="dbSNP:540780"
variation	1663184
	/allele="A"
	/allele="T"
	/db_xref="dbSNP:873713"
variation	1663484
	/allele="T"
	/allele="A"
	/db_xref="dbSNP:1006160"
variation	1663614
	/allele="C"
	/allele="A"
	/db_xref="dbSNP:1006159"
variation	1663714
	/allele="G"
	/allele="C"
	/db_xref="dbSNP:1006158"
variation	1663978
	/allele="T"
	/allele="G"
	/db_xref="dbSNP:1320656"
variation	1664189
	/allele="T"

variation /allele="C"
/db_xref="dbSNP:948108"
1664297
/allele="C"
/allele="A"
/db_xref="dbSNP:553357"
variation 1664372
/allele="A"
/allele="C"
/db_xref="dbSNP:563721"
variation 1664774
/allele="G"
/allele="T"
/db_xref="dbSNP:477957"
variation 1665016
/allele="G"
/allele="T"
/db_xref="dbSNP:479914"
variation 1665353
/allele="T"
/allele="G"
/db_xref="dbSNP:876797"
variation 1665660
/allele="G"
/allele="A"
/db_xref="dbSNP:876798"
variation 1666310
/allele="T"
/allele="C"
/db_xref="dbSNP:2155197"
variation 1666330
/allele="G"
/allele="A"
/db_xref="dbSNP:1892937"
variation 1666365
/allele="G"
/allele="A"
/db_xref="dbSNP:2155196"
variation 1667148
/allele="C"
/allele="T"
/db_xref="dbSNP:2155111"
variation 1668729
/allele="C"
/allele="A"
/db_xref="dbSNP:1269495"
variation 1668788
/allele="C"
/allele="A"
/db_xref="dbSNP:1272327"
variation 1671457
/allele="T"
/allele="G"
/db_xref="dbSNP:948107"
variation 1672459
/allele="G"
/allele="A"
/db_xref="dbSNP:497190"
STS 1673554..1673890
/standard_name="GDB:315997"

```
variation /note="WARNING: map location ambiguous"
          /db_xref="UniSTS:156559"
          1675217
          /allele="G"
          /allele="A"
          /db_xref="dbSNP:476130"
variation 1675365
          /allele="A"
          /allele="C"
          /db_xref="dbSNP:565530"
variation 1676403
          /allele="T"
          /allele="C"
          /db_xref="dbSNP:555577"
variation 1676626
          /allele="G"
          /allele="A"
          /db_xref="dbSNP:553709"
variation 1676673
          /allele="G"
          /allele="A"
          /db_xref="dbSNP:531855"
variation 1677767
          /allele="G"
          /allele="A"
          /db_xref="dbSNP:500787"
STS       1680234..1680579
          /standard_name="SHGC-143196"
          /db_xref="UniSTS:174071"
variation 1680385
          /allele="G"
          /allele="A"
          /db_xref="dbSNP:496371"
variation 1680513
          /allele="G"
          /allele="A"
          /db_xref="dbSNP:686245"
variation 1680613
          /allele="T"
          /allele="C"
          /db_xref="dbSNP:498314"
variation 1682927
          /allele="C"
          /allele="T"
          /db_xref="dbSNP:556028"
variation 1683202
          /allele="T"
          /allele="C"
          /db_xref="dbSNP:558680"
variation 1683495
          /allele="T"
          /allele="C"
          /db_xref="dbSNP:561394"
variation 1683784
          /allele="G"
          /allele="A"
          /db_xref="dbSNP:1244225"
variation 1683939
          /allele="A"
          /allele="C"
```

```

variation      /db_xref="dbSNP:624637"
                1683955
                /allele="C"
                /allele="A"
variation      /db_xref="dbSNP:624652"
                1684220
                /allele="T"
                /allele="C"
variation      /db_xref="dbSNP:512481"
                1684656
                /allele="T"
                /allele="C"
variation      /db_xref="dbSNP:1244223"
                1686647
                /allele="G"
                /allele="A"
variation      /db_xref="dbSNP:1145223"
                1689520
                /allele="T"
                /allele="G"
variation      /db_xref="dbSNP:581089"
                1689543
                /allele="T"
                /allele="G"
gene           /db_xref="dbSNP:663694"
                1689604..1695407
                /gene="FXVD6"
                /db_xref="LocusID:53826"
mRNA          join(1689604..1689666,1690357..1690395,1690520..1690594,
                1691201..1691237,1692017..1692066,1692555..1692604,
                1694108..1695407)
                /gene="FXVD6"
                /product="FXVD domain-containing ion transport regulator
                6"
                /note="Derived by automated computational analysis.
                Supporting evidence includes similarity to: 1 mRNA"
                /transcript_id="XM_052097.2"
                /db_xref="GI:15314334"
                /db_xref="LocusID:53826"
CDS           join(1689609..1689666,1690357..1690395,1690520..1690594,
                1691201..1691237,1692017..1692066,1692555..1692583)
                /gene="FXVD6"
                /codon_start=1
                /protein_id="XP_052097.1"
                /db_xref="GI:14774248"
                /db_xref="LocusID:53826"
variation      1690213
                /gene="FXVD6"
                /allele="T"
                /allele="C"
variation      /db_xref="dbSNP:473057"
                1691538
                /gene="FXVD6"
                /allele="G"
                /allele="A"
variation      /db_xref="dbSNP:519991"
                1691868
                /gene="FXVD6"
                /allele="T"
                /allele="C"

```

```
variation      /db_xref="dbSNP:496164"
               1692982
               /gene="FXVD6"
               /allele="T"
               /allele="G"
variation      /db_xref="dbSNP:562089"
               1693346
               /gene="FXVD6"
               /allele="G"
               /allele="A"
variation      /db_xref="dbSNP:564989"
               1694072
               /gene="FXVD6"
               /allele="T"
               /allele="C"
variation      /db_xref="dbSNP:516655"
               1694475
               /gene="FXVD6"
               /allele="C"
               /allele="T"
variation      /db_xref="dbSNP:520333"
               1694525
               /gene="FXVD6"
               /allele="C"
               /allele="A"
variation      /db_xref="dbSNP:506002"
               1694565
               /gene="FXVD6"
               /note="WARNING: map location ambiguous"
               /allele="C"
               /allele="G"
variation      /db_xref="dbSNP:1042978"
               1694766
               /gene="FXVD6"
               /note="WARNING: map location ambiguous"
               /allele="C"
               /allele="T"
STS            /db_xref="dbSNP:1042980"
               1694876..1695043
               /gene="FXVD6"
               /standard_name="SHGC-525"
               /note="WARNING: map location ambiguous"
STS            /db_xref="UniSTS:14718"
               1694957..1695044
               /gene="FXVD6"
               /standard_name="D11S943E"
               /note="WARNING: map location ambiguous"
STS            /db_xref="UniSTS:26469"
               1694975..1695083
               /gene="FXVD6"
               /standard_name="D11S2293E"
               /note="WARNING: map location ambiguous"
STS            /db_xref="UniSTS:68022"
               1695144..1695369
               /gene="FXVD6"
               /standard_name="stSG1265"
               /note="WARNING: map location ambiguous"
variation      /db_xref="UniSTS:75935"
               1700995
               /note="WARNING: map location ambiguous"
```



```

variation    /allele="A"
              /allele="C"
              /db_xref="dbSNP:2186666"
              1702438
              /note="WARNING: map location ambiguous"
              /allele="A"
              /allele="C"
              /db_xref="dbSNP:677928"
variation    1702447
              /note="WARNING: map location ambiguous"
              /allele="A"
              /allele="C"
              /db_xref="dbSNP:677938"
variation    1702501
              /note="WARNING: map location ambiguous"
              /allele="G"
              /allele="T"
              /db_xref="dbSNP:527466"
variation    1702569
              /note="WARNING: map location ambiguous"
              /allele="G"
              /allele="T"
              /db_xref="dbSNP:678457"
variation    1702584
              /note="WARNING: map location ambiguous"
              /allele="G"
              /allele="T"
              /db_xref="dbSNP:678806"
gene         1704305..1712242
              /gene="FXVD2"
              /note="synonyms: HOMG2, ATP1G1"
              /db_xref="LocusID:486"
              /db_xref="MIM:601814"
mRNA         join(1704305..1704390,1709668..1709706,1709905..1709979,
              1711490..1711526,1711689..1711719,1712013..1712242)
              /gene="FXVD2"
              /product="FXVD domain-containing ion transport regulator
              2"
              /note="Derived by automated computational analysis.
              Supporting evidence includes similarity to: 1 mRNA"
              /transcript_id="XM_052096.1"
              /db_xref="GI:14774243"
              /db_xref="LocusID:486"
              /db_xref="MIM:601814"
CDS          join(1704372..1704390,1709668..1709706,1709905..1709979,
              1711490..1711526,1711689..1711713)
              /gene="FXVD2"
              /codon_start=1
              /protein_id="XP_052096.1"
              /db_xref="GI:14774244"
              /db_xref="LocusID:486"
              /db_xref="MIM:601814"
STS          1705136..1705335
              /gene="FXVD2"
              /standard_name="SHGC-132239"
              /db_xref="UniSTS:170724"
STS          1705184..1705340
              /gene="FXVD2"
              /standard_name="D11S1998"
              /db_xref="UniSTS:13280"

```

```

variation      1706142
                /gene="FXVD2"
                /allele="A"
                /allele="G"
                /db_xref="dbSNP:479991"
variation      1706356
                /gene="FXVD2"
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:678776"
variation      1706380
                /gene="FXVD2"
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:514527"
variation      1707166
                /gene="FXVD2"
                /allele="G"
                /allele="T"
                /db_xref="dbSNP:1985658"
mRNA           join(1707675..1707731,1709668..1709706,1709905..1709979,
                1711490..1711526,1711689..1711719,1712013..1712242)
                /gene="FXVD2"
                /product="FXVD domain-containing ion transport regulator
                2"
                /note="Derived by automated computational analysis.
                Supporting evidence includes similarity to: 2 mRNAs"
                /transcript_id="XM_052095.1"
                /db_xref="GI:14774239"
                /db_xref="LocusID:486"
                /db_xref="MIM:601814"
CDS            join(1707707..1707731,1709668..1709706,1709905..1709979,
                1711490..1711526,1711689..1711713)
                /gene="FXVD2"
                /codon_start=1
                /protein_id="XP_052095.1"
                /db_xref="GI:14774240"
                /db_xref="LocusID:486"
                /db_xref="MIM:601814"
variation      1708850
                /gene="FXVD2"
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:636566"
variation      1709011
                /gene="FXVD2"
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:635706"
variation      1709845
                /gene="FXVD2"
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:529623"
variation      1710706
                /gene="FXVD2"
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:501171"
variation      1711044

```

```

/ gene="FXVD2"
/ allele="C"
/ allele="T"
/ db_xref="dbSNP:869790"
variation 1711072
/ gene="FXVD2"
/ allele="C"
/ allele="G"
/ db_xref="dbSNP:869791"
variation 1711714
/ gene="FXVD2"
/ allele="T"
/ allele="C"
/ db_xref="dbSNP:869789"
variation 1711952
/ gene="FXVD2"
/ allele="G"
/ allele="A"
/ db_xref="dbSNP:2014537"
variation 1711955
/ gene="FXVD2"
/ allele="G"
/ allele="A"
/ db_xref="dbSNP:2014536"
STS 1712100..1712223
/ gene="FXVD2"
/ standard_name="stSG26073"
/ db_xref="UniSTS:62045"
variation 1712182
/ gene="FXVD2"
/ allele="T"
/ allele="G"
/ db_xref="dbSNP:11999"
variation 1712604
/ allele="G"
/ allele="C"
/ db_xref="dbSNP:588807"
variation 1713551
/ allele="A"
/ allele="C"
/ db_xref="dbSNP:527534"
misc_feature 1713739..1885485
/ standard_name="RP11-35P15"
/ note="FISH-mapped clone"
/ map="11q23 (FHCRC) "
variation 1714202
/ allele="C"
/ allele="T"
/ db_xref="dbSNP:540442"
variation 1714875
/ allele="C"
/ allele="G"
/ db_xref="dbSNP:610226"
variation 1715688
/ allele="C"
/ allele="A"
/ db_xref="dbSNP:2077620"
variation 1715980
/ allele="G"
/ allele="A"

```

variation	/db_xref="dbSNP:2226635" 1716271 /allele="G" /allele="A"
variation	/db_xref="dbSNP:1939976" 1716440 /allele="A" /allele="G"
variation	/db_xref="dbSNP:1939219" 1716906 /allele="C" /allele="T"
variation	/db_xref="dbSNP:954319" 1719653 /allele="G" /allele="A"
variation	/db_xref="dbSNP:1145222" 1721989 /allele="G" /allele="A"
variation	/db_xref="dbSNP:495279" 1729876 /allele="T" /allele="C"
variation	/db_xref="dbSNP:591635" 1732347 /allele="T" /allele="C"
variation	/db_xref="dbSNP:657389" 1732354 /allele="G" /allele="A"
variation	/db_xref="dbSNP:657385" 1732443 /allele="T" /allele="A"
variation	/db_xref="dbSNP:2186626" 1733305 /allele="C" /allele="A"
variation	/db_xref="dbSNP:1892902" 1733480 /allele="G" /allele="A"
variation	/db_xref="dbSNP:1892903" 1736387 /allele="C" /allele="T"
variation	/db_xref="dbSNP:565312" 1738462 /allele="G" /allele="T"
variation	/db_xref="dbSNP:515701" 1738485 /allele="G" /allele="T"
variation	/db_xref="dbSNP:580842" 1738722 /allele="G" /allele="T"

variation /db_xref="dbSNP:573258"
1740190
/allele="G"
/allele="T"
variation /db_xref="dbSNP:528431"
1740851
/allele="A"
/allele="G"
variation /db_xref="dbSNP:534761"
1741365
/allele="G"
/allele="C"
variation /db_xref="dbSNP:1014034"
1741999
/allele="A"
/allele="G"
variation /db_xref="dbSNP:625447"
1742521
/allele="G"
/allele="T"
variation /db_xref="dbSNP:948099"
1742824
/allele="C"
/allele="G"
variation /db_xref="dbSNP:948100"
1746325
/allele="A"
/allele="G"
STS /db_xref="dbSNP:715315"
1746398..1746694
/standard_name="SHGC-141970"
/db_xref="UniSTS:171167"
variation 1746789
/allele="C"
/allele="T"
variation /db_xref="dbSNP:948102"
1748923
/allele="T"
/allele="G"
variation /db_xref="dbSNP:2155387"
1755257
/allele="A"
/allele="G"
STS /db_xref="dbSNP:1939368"
1758232..1758509
/standard_name="SHGC-105111"
/db_xref="UniSTS:169124"
STS 1758664..1758946
/standard_name="SHGC-152433"
/db_xref="UniSTS:137674"
STS 1758796..1758890
/standard_name="D11S4127"
/db_xref="UniSTS:19239"
variation 1772399
/allele="A"
/allele="G"
variation /db_xref="dbSNP:2155385"
1772408
/allele="G"
/allele="T"

variation	/db_xref="dbSNP:2155386" 1779042 /allele="C" /allele="T"
variation	/db_xref="dbSNP:2015482" 1781083 /allele="G" /allele="T"
variation	/db_xref="dbSNP:948101" 1782002 /allele="C" /allele="T"
variation	/db_xref="dbSNP:2105634" 1785721 /allele="A" /allele="G"
variation	/db_xref="dbSNP:1893038" 1787453 /allele="A" /allele="G"
variation	/db_xref="dbSNP:2077448" 1787598 /allele="C" /allele="T"
variation	/db_xref="dbSNP:748771" 1787929 /allele="G" /allele="A"
variation	/db_xref="dbSNP:869006" 1788304 /allele="G" /allele="A"
variation	/db_xref="dbSNP:869005" 1788380 /allele="C" /allele="T"
variation	/db_xref="dbSNP:1939977" 1791917 /allele="A" /allele="G"
variation	/db_xref="dbSNP:1939978" 1791938 /allele="A" /allele="G"
variation	/db_xref="dbSNP:1939979" 1791943 /allele="C" /allele="G"
variation	/db_xref="dbSNP:1939980" 1792246 /allele="T" /allele="C"
variation	/db_xref="dbSNP:1942931" 1794487 /allele="A" /allele="G"
variation	/db_xref="dbSNP:1939981" 1795962 /allele="G" /allele="A"

variation	/db_xref="dbSNP:1942930" 1797526 /allele="C" /allele="T"
variation	/db_xref="dbSNP:1939982" 1798002 /allele="G" /allele="A"
variation	/db_xref="dbSNP:1942929" 1798054 /allele="T" /allele="C"
variation	/db_xref="dbSNP:1942928" 1798871 /allele="C" /allele="G"
variation	/db_xref="dbSNP:1939983" 1798942 /allele="A" /allele="T"
STS	/db_xref="dbSNP:1939984" 1799378..1799477 /standard_name="SGC30873"
variation	/db_xref="UniSTS:720" 1805440 /allele="A" /allele="G"
variation	/db_xref="dbSNP:734378" 1805725 /allele="G" /allele="T"
variation	/db_xref="dbSNP:948103" 1806173 /allele="A" /allele="C"
variation	/db_xref="dbSNP:948104" 1807014 /allele="C" /allele="T"
variation	/db_xref="dbSNP:1893035" 1807183 /allele="C" /allele="T"
variation	/db_xref="dbSNP:1893036" 1809577 /allele="A" /allele="T"
variation	/db_xref="dbSNP:2212486" 1809623 /allele="C" /allele="T"
variation	/db_xref="dbSNP:2226634" 1809745 /allele="A" /allele="G"
variation	/db_xref="dbSNP:1893037" 1810363 /allele="A" /allele="C"
	/db_xref="dbSNP:1273019"

variation 1811446
/allele="A"
/allele="T"
/db_xref="dbSNP:948105"

variation 1811516
/allele="A"
/allele="G"
/db_xref="dbSNP:948106"

variation 1812189
/allele="C"
/allele="G"
/db_xref="dbSNP:948772"

variation 1816158
/allele="C"
/allele="T"
/db_xref="dbSNP:948773"

variation 1816219
/allele="A"
/allele="T"
/db_xref="dbSNP:948774"

variation 1816402
/allele="A"
/allele="G"
/db_xref="dbSNP:948775"

variation 1816477
/allele="G"
/allele="T"
/db_xref="dbSNP:948776"

variation 1816770
/allele="A"
/allele="G"
/db_xref="dbSNP:2187181"

variation 1818339
/allele="A"
/allele="C"
/db_xref="dbSNP:2187182"

variation 1818360
/allele="C"
/allele="T"
/db_xref="dbSNP:2187183"

variation 1818732
/allele="A"
/allele="G"
/db_xref="dbSNP:2156233"

variation 1821046
/allele="A"
/allele="G"
/db_xref="dbSNP:948777"

variation 1821315
/allele="G"
/allele="T"
/db_xref="dbSNP:693992"

variation 1821328
/allele="A"
/allele="C"
/db_xref="dbSNP:629060"

variation 1821411
/allele="A"
/allele="G"
/db_xref="dbSNP:588930"

variation 1821860
/allele="C"
/allele="G"
/db_xref="dbSNP:601503"

variation 1821872
/allele="A"
/allele="C"
/db_xref="dbSNP:641569"

variation 1822515
/allele="C"
/allele="T"
/db_xref="dbSNP:604245"

variation 1822591
/allele="C"
/allele="T"
/db_xref="dbSNP:655086"

variation 1822744
/allele="A"
/allele="G"
/db_xref="dbSNP:605500"

variation 1823285
/allele="A"
/allele="G"
/db_xref="dbSNP:634416"

variation 1823830
/allele="C"
/allele="T"
/db_xref="dbSNP:670972"

variation 1825176
/allele="A"
/allele="G"
/db_xref="dbSNP:656777"

variation 1825426
/allele="C"
/allele="T"
/db_xref="dbSNP:668213"

variation 1827105
/allele="C"
/allele="T"
/db_xref="dbSNP:685961"

variation 1827259
/allele="A"
/allele="G"
/db_xref="dbSNP:585718"

STS 1828615..1828916
/standard_name="SHGC-100726"
/db_xref="UniSTS:132790"

variation 1828703
/allele="G"
/allele="A"
/db_xref="dbSNP:650162"

variation 1828804
/allele="T"
/allele="C"
/db_xref="dbSNP:2068412"

variation 1830167
/allele="T"
/allele="A"
/db_xref="dbSNP:879951"

variation 1832249

variation /allele="G"
/allele="A"
/db_xref="dbSNP:603377"
1834282
/allele="G"
/allele="A"
/db_xref="dbSNP:1261819"
STS 1837764..1837897
/standard_name="SHGC-6188"
/db_xref="UniSTS:4898"
STS 1839791..1840020
/standard_name="SHGC-6010"
/db_xref="UniSTS:34898"
STS 1839909..1840051
/standard_name="D11S2060"
/db_xref="UniSTS:56279"
variation 1845214
/allele="C"
/allele="A"
/db_xref="dbSNP:721487"
variation 1845560
/allele="T"
/allele="C"
/db_xref="dbSNP:721486"
variation 1845720
/allele="A"
/allele="G"
/db_xref="dbSNP:1939234"
STS 1847960..1848109
/standard_name="WI-14137"
/db_xref="UniSTS:20289"
variation 1848762
/allele="C"
/allele="A"
/db_xref="dbSNP:1942924"
variation 1849039
/allele="G"
/allele="A"
/db_xref="dbSNP:1942923"
variation 1854242
/allele="C"
/allele="T"
/db_xref="dbSNP:637454"
variation 1854374
/allele="A"
/allele="G"
/db_xref="dbSNP:596440"
variation 1856249
/allele="G"
/allele="T"
/db_xref="dbSNP:608076"
variation 1856275
/allele="G"
/allele="T"
/db_xref="dbSNP:608049"
variation 1856340
/allele="T"
/allele="G"
/db_xref="dbSNP:607658"
variation 1857077

	/allele="T"
	/allele="G"
variation	/db_xref="dbSNP:656449"
	1858120
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:736491"
	1858625
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:686977"
	1860016
	/allele="T"
	/allele="A"
variation	/db_xref="dbSNP:682723"
	1860747
	/allele="T"
	/allele="C"
variation	/db_xref="dbSNP:658274"
	1861523
	/allele="T"
	/allele="C"
variation	/db_xref="dbSNP:688415"
	1861579
	/allele="T"
	/allele="A"
variation	/db_xref="dbSNP:688790"
	1863385
	/allele="T"
	/allele="G"
variation	/db_xref="dbSNP:636783"
	1863622
	/allele="T"
	/allele="G"
variation	/db_xref="dbSNP:947926"
	1864334
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:593380"
	1864647
	/allele="T"
	/allele="C"
variation	/db_xref="dbSNP:581580"
	1865041
	/allele="T"
	/allele="C"
variation	/db_xref="dbSNP:608811"
	1865301
	/allele="A"
	/allele="C"
variation	/db_xref="dbSNP:1145219"
	1865390
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:686413"
	1867010
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:687100"
	1867199

variation /allele="T"
/allele="C"
/db_xref="dbSNP:657364"
1868747
/allele="T"
/allele="G"
/db_xref="dbSNP:630024"
variation 1871139
/allele="T"
/allele="A"
/db_xref="dbSNP:594306"
variation 1871213
/allele="T"
/allele="A"
/db_xref="dbSNP:643758"
variation 1871635
/allele="T"
/allele="G"
/db_xref="dbSNP:1892918"
variation 1873478
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:621188"
STS 1874604..1874814
/standard_name="D11S2829"
/note="WARNING: map location ambiguous"
/db_xref="UniSTS:152017"
variation 1874724
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:671553"
variation 1877120
/allele="C"
/allele="T"
/db_xref="dbSNP:1941389"
variation 1877975
/allele="A"
/allele="G"
/db_xref="dbSNP:583983"
variation 1878645
/note="WARNING: map location ambiguous"
/allele="T"
/allele="G"
/db_xref="dbSNP:684669"
variation 1880863
/allele="C"
/allele="T"
/db_xref="dbSNP:1893517"
STS 1881103..1881452
/standard_name="AffySTS000113"
/db_xref="UniSTS:117800"
variation 1881133
/allele="G"
/allele="A"
/db_xref="dbSNP:16867"
STS 1881218..1881448
/standard_name="SHGC-130536"
/db_xref="UniSTS:137066"

```

variation      1881497
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:678327"
variation      1881596
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:1941392"
variation      1881683
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:610552"
variation      1881685
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:1941391"
STS            1883200..1883402
                /standard_name="D11S4092"
                /db_xref="UniSTS:53492"
variation      1883824
                /allele="A"
                /allele="T"
                /db_xref="dbSNP:610466"
variation      1884900
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:673028"
variation      1885062
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:626571"
variation      1885679
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:537592"
variation      1885737
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:536761"
variation      1888951
                /note="WARNING: map location ambiguous"
                /allele="G"
                /allele="C"
                /db_xref="dbSNP:236918"
STS            1889205..1889301
                /standard_name="SHGC-58052"
                /note="WARNING: map location ambiguous"
                /db_xref="UniSTS:33042"
variation      1889271
                /note="WARNING: map location ambiguous"
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:236917"
variation      1890002
                /note="WARNING: map location ambiguous"
                /allele="A"
                /allele="G"
                /db_xref="dbSNP:74830"
variation      1890838
                /note="WARNING: map location ambiguous"

```

variation /allele="C"
/allele="G"
/db_xref="dbSNP:2239009"
1890932
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:236916"
variation 1891554
/note="WARNING: map location ambiguous"
/allele="C"
/allele="G"
/db_xref="dbSNP:2239010"
variation 1891566
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
/db_xref="dbSNP:2239011"
variation 1892110
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:236915"
variation 1892198
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
/db_xref="dbSNP:2239012"
variation 1892477
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
/db_xref="dbSNP:2238005"
variation 1892767
/note="WARNING: map location ambiguous"
/allele="G"
/allele="T"
/db_xref="dbSNP:2238006"
variation 1893992
/note="WARNING: map location ambiguous"
/allele="C"
/allele="G"
/db_xref="dbSNP:947918"
variation 1899786
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:563838"
variation 1900226
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
/db_xref="dbSNP:507133"
variation 1900573
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
/db_xref="dbSNP:624555"
variation 1901144
/note="WARNING: map location ambiguous"

variation /allele="C"
/allele="A"
/db_xref="dbSNP:530012"
1901424
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
/db_xref="dbSNP:527347"
variation 1906357
/note="WARNING: map location ambiguous"
/allele="A"
/allele="T"
/db_xref="dbSNP:694696"
variation 1906949
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:560789"
variation 1907132
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:486366"
variation 1907177
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:558854"
STS 1908267..1908601
/standard_name="D11S3585"
/note="WARNING: map location ambiguous"
/db_xref="UniSTS:152824"
variation 1908313
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:564674"
variation 1908983
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
/db_xref="dbSNP:537323"
variation 1909224
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:535366"
variation 1910369
/note="WARNING: map location ambiguous"
/allele="T"
/allele="A"
/db_xref="dbSNP:542900"
variation 1910381
/note="WARNING: map location ambiguous"
/allele="T"
/allele="A"
/db_xref="dbSNP:542869"
variation 1910395
/note="WARNING: map location ambiguous"
/allele="C"

variation /allele="A"
/db_xref="dbSNP:542176"
1910702
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
variation /db_xref="dbSNP:654479"
1910803
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
variation /db_xref="dbSNP:499744"
1910949
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
variation /db_xref="dbSNP:553506"
1910958
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
variation /db_xref="dbSNP:655389"
1911018
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
variation /db_xref="dbSNP:553303"
1911470
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
variation /db_xref="dbSNP:657666"
1912137
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
variation /db_xref="dbSNP:521329"
1913695
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
variation /db_xref="dbSNP:688207"
1913883
/note="WARNING: map location ambiguous"
/allele="C"
/allele="A"
variation /db_xref="dbSNP:484490"
1923405
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
variation /db_xref="dbSNP:476983"
1926628
/note="WARNING: map location ambiguous"
/allele="C"
/allele="A"
variation /db_xref="dbSNP:693357"
1927734
/note="WARNING: map location ambiguous"
/allele="T"

variation /allele="C"
/db_xref="dbSNP:516742"
1927740
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:516712"
variation 1928382
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
/db_xref="dbSNP:1784045"
variation 1928664
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
/db_xref="dbSNP:675228"
variation 1928674
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:495626"
variation 1928679
/note="WARNING: map location ambiguous"
/allele="G"
/allele="C"
/db_xref="dbSNP:495618"
variation 1932368
/allele="A"
/allele="G"
/db_xref="dbSNP:1939235"
variation 1933886
/allele="A"
/allele="G"
/db_xref="dbSNP:568221"
variation 1934093
/allele="A"
/allele="G"
/db_xref="dbSNP:666290"
STS 1934418..1934559
/standard_name="D11S2472"
/db_xref="UniSTS:14441"
variation 1934894
/allele="A"
/allele="C"
/db_xref="dbSNP:680292"
variation 1935002
/allele="A"
/allele="G"
/db_xref="dbSNP:680730"
variation 1935183
/allele="A"
/allele="T"
/db_xref="dbSNP:490914"
variation 1936402
/allele="G"
/allele="T"
/db_xref="dbSNP:1263889"
variation 1938037
/allele="A"

	/allele="T"
	/db_xref="dbSNP:579720"
variation	1938435
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:577651"
variation	1940436
	/allele="C"
	/allele="A"
	/db_xref="dbSNP:1893971"
variation	1940670
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:748316"
variation	1941466
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:622860"
variation	1942866
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:2186761"
variation	1946087
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:694005"
variation	1946197
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:649233"
variation	1947260
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:498689"
variation	1948385
	/allele="A"
	/allele="C"
	/db_xref="dbSNP:551554"
variation	1948658
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:553637"
variation	1948684
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:647593"
variation	1950137
	/allele="G"
	/allele="C"
	/db_xref="dbSNP:634406"
variation	1950230
	/allele="G"
	/allele="C"
	/db_xref="dbSNP:633985"
variation	1950232
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:633983"
variation	1950598
	/allele="A"

	/allele="G"
	/db_xref="dbSNP:498889"
variation	1950992
	/allele="G"
	/allele="T"
	/db_xref="dbSNP:1962032"
STS	1951444..1951769
	/standard_name="SHGC-144571"
	/db_xref="UniSTS:182404"
variation	1951721
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:600620"
variation	1953900
	/allele="G"
	/allele="C"
	/db_xref="dbSNP:495420"
variation	1954226
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:654946"
variation	1954591
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:474749"
variation	1955101
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:1940036"
variation	1955190
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:1940035"
variation	1955627
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:638979"
variation	1956392
	/allele="T"
	/allele="G"
	/db_xref="dbSNP:608093"
variation	1958048
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:681046"
variation	1958724
	/allele="G"
	/allele="C"
	/db_xref="dbSNP:684973"
variation	1958944
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:537997"
variation	1959166
	/allele="T"
	/allele="A"
	/db_xref="dbSNP:536031"
variation	1959828
	/allele="T"
	/allele="G"

variation /db_xref="dbSNP:669226"
1962887
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"

variation /db_xref="dbSNP:648740"
1963229
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"

variation /db_xref="dbSNP:505824"
1963315
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"

variation /db_xref="dbSNP:504935"
1965002
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"

variation /db_xref="dbSNP:557396"
1966216
/allele="C"
/allele="T"

variation /db_xref="dbSNP:746910"
1966904
/allele="T"
/allele="G"

variation /db_xref="dbSNP:730302"
1967872
/allele="G"
/allele="C"

variation /db_xref="dbSNP:2017098"
1968018
/allele="G"
/allele="C"

variation /db_xref="dbSNP:87824"
1968639
/allele="C"
/allele="G"

variation /db_xref="dbSNP:680424"
1968765
/allele="A"
/allele="G"

variation /db_xref="dbSNP:657137"
1968867
/allele="C"
/allele="T"

variation /db_xref="dbSNP:557940"
1969649
/allele="C"
/allele="G"

variation /db_xref="dbSNP:629397"
1969993
/allele="T"
/allele="C"

variation /db_xref="dbSNP:631120"
1970089
/allele="C"
/allele="T"

variation /db_xref="dbSNP:479601"
1973324
/allele="A"
/allele="C"
variation /db_xref="dbSNP:1893899"
1973354
/allele="A"
/allele="G"
variation /db_xref="dbSNP:1893900"
1974070
/allele="A"
/allele="G"
variation /db_xref="dbSNP:490458"
1974165
/allele="A"
/allele="G"
variation /db_xref="dbSNP:1940037"
1975275
/allele="C"
/allele="G"
variation /db_xref="dbSNP:752795"
1975277
/allele="C"
/allele="T"
variation /db_xref="dbSNP:752796"
1975532
/allele="C"
/allele="T"
STS /db_xref="dbSNP:495118"
1975633..1975882
/standard_name="D11S1091"
/db_xref="UniSTS:29698"
variation 1976045
/allele="T"
/allele="C"
variation /db_xref="dbSNP:685916"
1976295
/allele="C"
/allele="T"
variation /db_xref="dbSNP:522742"
1976521
/allele="A"
/allele="G"
variation /db_xref="dbSNP:2010473"
1976574
/allele="G"
/allele="T"
variation /db_xref="dbSNP:755791"
1977183
/allele="G"
/allele="A"
variation /db_xref="dbSNP:2010508"
1977826
/allele="A"
/allele="G"
variation /db_xref="dbSNP:1893969"
1978226
/allele="A"
/allele="G"
/db_xref="dbSNP:1893970"

variation 1978552
/allele="A"
/allele="G"
/db_xref="dbSNP:475422"

variation 1979215
/allele="C"
/allele="T"
/db_xref="dbSNP:623052"

variation 1979289
/allele="C"
/allele="G"
/db_xref="dbSNP:503281"

variation 1979329
/allele="C"
/allele="T"
/db_xref="dbSNP:567053"

variation 1979419
/allele="C"
/allele="T"
/db_xref="dbSNP:567988"

variation 1980532
/allele="A"
/allele="G"
/db_xref="dbSNP:685425"

variation 1980542
/allele="A"
/allele="C"
/db_xref="dbSNP:685440"

variation 1981226
/allele="T"
/allele="C"
/db_xref="dbSNP:479591"

variation 1981982
/allele="C"
/allele="T"
/db_xref="dbSNP:562422"

variation 1983717
/allele="C"
/allele="T"
/db_xref="dbSNP:490111"

variation 1985251
/allele="G"
/allele="A"
/db_xref="dbSNP:579239"

variation 1985257
/allele="C"
/allele="T"
/db_xref="dbSNP:665218"

variation 1986255
/allele="C"
/allele="T"
/db_xref="dbSNP:576390"

variation 1986324
/allele="C"
/allele="G"
/db_xref="dbSNP:686598"

variation 1986722
/allele="G"
/allele="T"
/db_xref="dbSNP:580714"

variation 1987618
/allele="G"
/allele="A"
/db_xref="dbSNP:640147"

variation 1987998
/allele="C"
/allele="A"
/db_xref="dbSNP:599411"

variation 1988276
/allele="T"
/allele="C"
/db_xref="dbSNP:565083"

variation 1988402
/allele="T"
/allele="C"
/db_xref="dbSNP:636530"

variation 1988436
/allele="T"
/allele="C"
/db_xref="dbSNP:542322"

variation 1988461
/allele="G"
/allele="C"
/db_xref="dbSNP:597583"

variation 1988835
/allele="C"
/allele="T"
/db_xref="dbSNP:553062"

variation 1989904
/allele="G"
/allele="A"
/db_xref="dbSNP:609353"

variation 1993352
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:521187"

variation 1995875
/allele="G"
/allele="A"
/db_xref="dbSNP:650535"

variation 1996230
/allele="C"
/allele="T"
/db_xref="dbSNP:563531"

variation 1996396
/allele="A"
/allele="G"
/db_xref="dbSNP:678468"

variation 1997189
/allele="T"
/allele="G"
/db_xref="dbSNP:533428"

variation 1997226
/allele="T"
/allele="G"
/db_xref="dbSNP:533331"

variation 1997639
/note="WARNING: map location ambiguous"
/allele="T"

```

/allele="C"
/db_xref="dbSNP:679223"
variation 1997807
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
variation 1998868
/db_xref="dbSNP:506836"
/allele="T"
/allele="C"
variation 1999219
/db_xref="dbSNP:525110"
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
variation 2002081
/db_xref="dbSNP:634867"
/allele="A"
/allele="G"
variation 2002104
/db_xref="dbSNP:661631"
/allele="G"
/allele="C"
variation 2002183
/db_xref="dbSNP:473343"
/allele="A"
/allele="G"
variation 2002959
/db_xref="dbSNP:557053"
/allele="T"
/allele="C"
variation 2003521
/db_xref="dbSNP:521609"
/allele="C"
/allele="G"
variation 2004564
/db_xref="dbSNP:688968"
/allele="T"
/allele="A"
variation 2006081
/db_xref="dbSNP:2076965"
/allele="A"
/allele="C"
gene 2007019..2111771
/db_xref="dbSNP:612979"
/gene="DSCAML1"
/note="synonym: KIAA1132"
mRNA 2007019..2007169,2014462..2014740,2018140..2018415,
2020783..2021170)
/gene="DSCAML1"
/product="Downs syndrome cell adhesion molecule like 1"
/note="Derived by automated computational analysis.
Supporting evidence includes similarity to: 1 mRNA"
/transcript_id="XM_052055.2"
variation 2007200
/db_xref="GI:15314347"
/db_xref="LocusID:57453"
/gene="DSCAML1"
/allele="A"

```


	/allele="C"
	/db_xref="dbSNP:550898"
variation	2013269
	/gene="DSCAML1"
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:1941390"
variation	2014147
	/gene="DSCAML1"
	/allele="G"
	/allele="T"



PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Bio

Search for

Limits

Preview/Index

History

Clipboard

Details

Show:

☐ 1: NT_024766[gi:18585923] This record was removed as a result of standard genome annotation processing. See the genome build documentation at <http://www.ncbi.nlm.nih.gov/genome/guide/build.html> for further information, or contact info@ncbi.nlm.nih.gov.

LOCUS NT_024766 531499 bp DNA linear CON 07-FEB-2002
 DEFINITION Homo sapiens chromosome 16 working draft sequence segment.
 ACCESSION NT_024766
 VERSION NT_024766.5 GI:18585923
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 531499)
 AUTHORS NCBI Annotation Project.
 TITLE Direct Submission
 JOURNAL Submitted (06-FEB-2002) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA
 COMMENT GENOME ANNOTATION REFSEQ: NCBI contigs are derived from assembled
 genomic sequence data.
 Also see:
 Documentation of NCBI's Annotation Process

On Feb 7, 2002 this sequence version replaced gi:14778846.
 COMPLETENESS: not full length.

FEATURES
 source Location/Qualifiers
 1..531499
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="16"
 gene 1266..10375
 /gene="LOC162126"
 /note="Located on Accession NT_024766"
 /db_xref="InterimID:162126"
 mRNA join(1266..1352, 2588..2668, 3441..3524, 3769..3882,
 5890..5973, 6589..6672, 10292..10375)
 /gene="LOC162126"
 /product="similar to hypothetical protein FLJ21709 (H.
 sapiens)"
 /note="Derived by automated computational analysis using
 gene prediction method: GenomeScan."
 /transcript_id="XM_102419.1"
 /db_xref="GI:18585915"
 /db_xref="InterimID:162126"
 CDS join(3501..3524, 3769..3804)
 /gene="LOC162126"
 /note="Located on Accession NT_024766"

variation /codon_start=1
/protein_id="XP_102419.1"
/db_xref="GI:18585916"
/db_xref="InterimID:162126"
4255
/gene="LOC162126"
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
/db_xref="dbSNP:289709"
variation 5721
/gene="LOC162126"
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
/db_xref="dbSNP:289710"
variation 5996
/gene="LOC162126"
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
/db_xref="dbSNP:289711"
variation 6879
/gene="LOC162126"
/allele="C"
/allele="G"
/db_xref="dbSNP:1624355"
variation 7623
/gene="LOC162126"
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
/db_xref="dbSNP:1645962"
variation 7824
/gene="LOC162126"
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
/db_xref="dbSNP:708271"
variation 8680
/gene="LOC162126"
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:247591"
variation 10388
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
/db_xref="dbSNP:1144773"
variation 10413
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
/db_xref="dbSNP:1144774"
variation 10462
/note="WARNING: map location ambiguous"
/allele="A"
/allele="C"
/db_xref="dbSNP:1144775"

```

variation      10774
                /allele="T"
                /allele="G"
                /db_xref="dbSNP:1672871"
variation      10779
                /allele="T"
                /allele="G"
                /db_xref="dbSNP:1672870"
variation      10793
                /allele="T"
                /allele="G"
                /db_xref="dbSNP:1672869"
gene           11712..29309
                /gene="FLJ21709"
                /note="Located on Accession NT_024766"
                /db_xref="LocusID:84166"
mRNA           join(11712..11801,13037..13117,13890..13973,14239..14331,
                16340..16423,17041..17124,20399..20482,22607..22690,
                23084..23167,23507..23590,23731..23808,24838..24921,
                25009..25080,25334..25417,26888..26971,27317..27400,
                28207..29309)
                /gene="FLJ21709"
                /product="hypothetical protein FLJ21709"
                /note="Derived by automated computational analysis using
                gene prediction method: BLAST. Supporting evidence
                includes similarity to: 2 mRNAs"
                /transcript_id="XM_027750.2"
                /db_xref="GI:18585899"
                /db_xref="LocusID:84166"
CDS           join(13942..13973,14239..14331,16340..16423,17041..17124,
                20399..20482,22607..22690,23084..23167,23507..23590,
                23731..23808,24838..24921,25009..25080,25334..25417,
                26888..26971,27317..27400,28207..28318)
                /gene="FLJ21709"
                /note="Located on Accession NT_024766"
                /codon_start=1
                /protein_id="XP_027750.2"
                /db_xref="GI:18585900"
                /db_xref="LocusID:84166"
variation      14704
                /gene="FLJ21709"
                /note="WARNING: map location ambiguous"
                /allele="A"
                /allele="G"
                /db_xref="dbSNP:289709"
variation      16171
                /gene="FLJ21709"
                /note="WARNING: map location ambiguous"
                /allele="A"
                /allele="G"
                /db_xref="dbSNP:289710"
variation      16446
                /gene="FLJ21709"
                /note="WARNING: map location ambiguous"
                /allele="C"
                /allele="T"
                /db_xref="dbSNP:289711"
variation      17326
                /gene="FLJ21709"
                /allele="G"

```

variation /allele="T"
/db_xref="dbSNP:1186013"
17378
/gene="FLJ21709"
/allele="A"
/allele="T"
variation /db_xref="dbSNP:1184852"
17403
/gene="FLJ21709"
/allele="A"
/allele="G"
variation /db_xref="dbSNP:1186221"
17705
/gene="FLJ21709"
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
variation /db_xref="dbSNP:1167429"
/db_xref="dbSNP:1645962"
17906
/gene="FLJ21709"
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
variation /db_xref="dbSNP:708271"
18427
/gene="FLJ21709"
/allele="A"
/allele="T"
variation /db_xref="dbSNP:2895451"
18783
/gene="FLJ21709"
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
variation /db_xref="dbSNP:247591"
19020
/gene="FLJ21709"
/allele="C"
/allele="G"
variation /db_xref="dbSNP:152221"
19447
/gene="FLJ21709"
/allele="C"
/allele="T"
variation /db_xref="dbSNP:149627"
19457
/gene="FLJ21709"
/allele="A"
/allele="G"
variation /db_xref="dbSNP:698244"
20495
/gene="FLJ21709"
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
variation /db_xref="dbSNP:1144773"
20520
/gene="FLJ21709"
/note="WARNING: map location ambiguous"

variation /allele="A"
 /allele="G"
 /db_xref="dbSNP:1144774"
20569
 /gene="FLJ21709"
 /note="WARNING: map location ambiguous"
 /allele="A"
 /allele="C"
 /db_xref="dbSNP:1144775"
variation 20681
 /gene="FLJ21709"
 /allele="G"
 /allele="A"
 /db_xref="dbSNP:1151267"
variation 20708
 /gene="FLJ21709"
 /allele="A"
 /allele="G"
 /db_xref="dbSNP:1011130"
variation 20722
 /gene="FLJ21709"
 /allele="T"
 /allele="G"
 /db_xref="dbSNP:1151268"
variation 20855
 /gene="FLJ21709"
 /allele="T"
 /allele="G"
 /db_xref="dbSNP:1684582"
variation 21380
 /gene="FLJ21709"
 /allele="C"
 /allele="T"
 /db_xref="dbSNP:37481"
variation 21562
 /gene="FLJ21709"
 /allele="C"
 /allele="T"
 /db_xref="dbSNP:27199"
variation 21995
 /gene="FLJ21709"
 /allele="G"
 /allele="T"
 /db_xref="dbSNP:27902"
variation 22878
 /gene="FLJ21709"
 /allele="T"
 /allele="C"
 /db_xref="dbSNP:41383"
variation 23320
 /gene="FLJ21709"
 /allele="C"
 /allele="T"
 /db_xref="dbSNP:27726"
variation 23701
 /gene="FLJ21709"
 /allele="T"
 /allele="C"
 /db_xref="dbSNP:27392"
variation 25105

	/gene="FLJ21709"
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:42221"
	25765
	/gene="FLJ21709"
	/allele="C"
	/allele="A"
variation	/db_xref="dbSNP:150366"
	25780
	/gene="FLJ21709"
	/allele="T"
	/allele="A"
variation	/db_xref="dbSNP:158484"
	26557
	/gene="FLJ21709"
	/allele="C"
	/allele="A"
variation	/db_xref="dbSNP:820944"
	26802
	/gene="FLJ21709"
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:154045"
	26860
	/gene="FLJ21709"
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:154044"
	27152
	/gene="FLJ21709"
	/allele="T"
	/allele="C"
variation	/db_xref="dbSNP:154043"
	27681
	/gene="FLJ21709"
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:154042"
	27914
	/gene="FLJ21709"
	/allele="C"
	/allele="A"
variation	/db_xref="dbSNP:150348"
	28165
	/gene="FLJ21709"
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:27195"
	28392
	/gene="FLJ21709"
	/allele="A"
	/allele="T"
variation	/db_xref="dbSNP:27194"
	28697
	/gene="FLJ21709"
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:43216"
STS	29163..29292

	/gene="FLJ21709"
	/standard_name="D16S3209"
	/db_xref="UniSTS:21082"
STS	29167..29299
	/gene="FLJ21709"
	/standard_name="RH65291"
	/db_xref="UniSTS:92066"
variation	29283
	/gene="FLJ21709"
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:27193"
variation	29394
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:27192"
variation	29729
	/allele="G"
	/allele="C"
	/db_xref="dbSNP:27191"
variation	30086
	/allele="G"
	/allele="C"
	/db_xref="dbSNP:27190"
variation	31750
	/allele="G"
	/allele="T"
	/db_xref="dbSNP:166254"
variation	31785
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:158618"
variation	32800
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:711756"
variation	33261
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:711757"
variation	34208
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:822113"
variation	34459
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:822114"
variation	34872
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:172336"
variation	36260
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:171571"
variation	36321
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:167051"


```

variation      36519
                /allele="C"
                /allele="T"
                /db_xref="dbSNP:711758"
variation      36709
                /allele="A"
                /allele="G"
                /db_xref="dbSNP:181789"
variation      37252
                /allele="A"
                /allele="G"
                /db_xref="dbSNP:289721"
variation      37282
                /allele="A"
                /allele="G"
                /db_xref="dbSNP:289722"
gene           38415..93767
                /gene="LOC113007"
                /note="Located on Accession NT_024766"
                /db_xref="InterimID:113007"
mRNA           join(38415..38590,56507..56721,59087..59266,61275..61349,
                63294..63366,64995..65078,65361..65450,66893..66991,
                67474..67560,69214..69273,71660..71793,73649..73703,
                80578..80629,82951..83084,91888..92124,93354..93767)
                /gene="LOC113007"
                /product="similar to Unknown (protein for MGC:16924)"
                /note="Derived by automated computational analysis using
                gene prediction method: BLAST. Supporting evidence
                includes similarity to: 1 mRNA"
                /transcript_id="XM_053605.3"
                /db_xref="GI:18585901"
                /db_xref="InterimID:113007"
variation      43190
                /gene="LOC113007"
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:1167428"
variation      52029
                /gene="LOC113007"
                /allele="G"
                /allele="C"
                /db_xref="dbSNP:1645957"
variation      53684
                /gene="LOC113007"
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:1672872"
variation      57015
                /gene="LOC113007"
                /allele="G"
                /allele="C"
                /db_xref="dbSNP:864798"
variation      57080
                /gene="LOC113007"
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:866627"
variation      57103
                /gene="LOC113007"
                /allele="G"

```

```

variation      /allele="T"
                /db_xref="dbSNP:2399617"
                57238
                /gene="LOC113007"
                /allele="G"
                /allele="A"
variation      /db_xref="dbSNP:714406"
                59275
                /gene="LOC113007"
                /allele="T"
                /allele="G"
variation      /db_xref="dbSNP:2305701"
                59409
                /gene="LOC113007"
                /allele="T"
                /allele="C"
variation      /db_xref="dbSNP:2305700"
                61532
                /gene="LOC113007"
                /allele="C"
                /allele="A"
variation      /db_xref="dbSNP:2305699"
                61865
                /gene="LOC113007"
                /allele="T"
                /allele="C"
variation      /db_xref="dbSNP:291053"
                62393
                /gene="LOC113007"
                /allele="C"
                /allele="A"
variation      /db_xref="dbSNP:158619"
                64491..64492
                /gene="LOC113007"
                /allele="-"
                /allele="GGAT"
variation      /db_xref="dbSNP:3054318"
                64907
                /gene="LOC113007"
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:2305698"
CDS            join(65058..65078,65361..65450,66893..66991,67474..67560,
                69214..69273,71660..71793,73649..73703,80578..80629,
                82951..83084,91888..92124,93354..93461)
                /gene="LOC113007"
                /note="Located on Accession NT_024766"
                /codon_start=1
                /protein_id="XP_053605.1"
                /db_xref="GI:15318878"
                /db_xref="InterimID:113007"
variation      66435
                /gene="LOC113007"
                /allele="C"
                /allele="A"
                /db_xref="dbSNP:1545614"
variation      66919
                /gene="LOC113007"
                /allele="T"
                /allele="C"

```

```

variation      /db_xref="dbSNP:2305697"
                68923
                /gene="LOC113007"
                /allele="T"
                /allele="G"
variation      /db_xref="dbSNP:2216758"
                69094
                /gene="LOC113007"
                /allele="T"
                /allele="C"
variation      /db_xref="dbSNP:2305696"
                71914
                /gene="LOC113007"
                /allele="T"
                /allele="C"
variation      /db_xref="dbSNP:2278985"
                72326
                /gene="LOC113007"
                /allele="T"
                /allele="A"
variation      /db_xref="dbSNP:173897"
                74320
                /gene="LOC113007"
                /allele="C"
                /allele="A"
variation      /db_xref="dbSNP:1895516"
                74544
                /gene="LOC113007"
                /allele="G"
                /allele="A"
variation      /db_xref="dbSNP:1895515"
                80326
                /gene="LOC113007"
                /allele="G"
                /allele="A"
variation      /db_xref="dbSNP:2305695"
                80542
                /gene="LOC113007"
                /allele="G"
                /allele="A"
gene           /db_xref="dbSNP:2305694"
                complement(82956..93758)
                /gene="LOC146470"
                /note="Located on Accession NT_024766"
mRNA          /db_xref="InterimID:146470"
                complement(join(82956..83084,91888..92124,93354..93758))
                /gene="LOC146470"
                /product="hypothetical gene LOC146470"
                /note="Derived by automated computational analysis using
                gene prediction method: BLAST."
                /transcript_id="XM_085481.1"
                /db_xref="GI:18585902"
                /db_xref="InterimID:146470"
CDS           complement(join(83003..83084,91888..92124,93354..93484))
                /gene="LOC146470"
                /note="Located on Accession NT_024766"
                /codon_start=1
                /protein_id="XP_085481.1"
                /db_xref="GI:18585903"
                /db_xref="InterimID:146470"

```

variation 83123
/gene="LOC113007"
/allele="G"
/allele="C"
/db_xref="dbSNP:2305693"

variation 83127
/gene="LOC113007"
/allele="T"
/allele="C"
/db_xref="dbSNP:2305692"

variation 83287
/gene="LOC113007"
/allele="T"
/allele="C"
/db_xref="dbSNP:2305691"

variation 83909
/gene="LOC113007"
/allele="G"
/allele="A"
/db_xref="dbSNP:1466294"

variation 84075
/gene="LOC113007"
/allele="T"
/allele="C"
/db_xref="dbSNP:1466293"

variation 84223
/gene="LOC113007"
/allele="A"
/allele="G"
/db_xref="dbSNP:735046"

variation 84519
/gene="LOC113007"
/allele="T"
/allele="C"
/db_xref="dbSNP:889558"

variation 84798
/gene="LOC113007"
/allele="C"
/allele="T"
/db_xref="dbSNP:2399618"

variation 84861
/gene="LOC113007"
/allele="G"
/allele="C"
/db_xref="dbSNP:169726"

variation 84898
/gene="LOC113007"
/allele="A"
/allele="T"
/db_xref="dbSNP:2399620"

variation 84901
/gene="LOC113007"
/allele="C"
/allele="G"
/db_xref="dbSNP:2399621"

variation 84970
/gene="LOC113007"
/allele="A"
/allele="G"
/db_xref="dbSNP:2399622"

```

variation      85519
                /gene="LOC113007"
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:2013644"
variation      85537
                /gene="LOC113007"
                /allele="G"
                /allele="C"
                /db_xref="dbSNP:2013641"
variation      85564
                /gene="LOC113007"
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:976977"
variation      86587
                /gene="LOC113007"
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:2445690"
STS            90911..91124
                /gene="LOC113007"
                /standard_name="SHGC-61122"
                /db_xref="UniSTS:3601"
STS            90939..91075
                /gene="LOC113007"
                /standard_name="RH64876"
                /db_xref="UniSTS:83563"
variation      92049
                /gene="LOC113007"
                /allele="C"
                /allele="A"
                /db_xref="dbSNP:2279407"
variation      92608
                /gene="LOC113007"
                /allele="T"
                /allele="G"
                /db_xref="dbSNP:2279406"
variation      93025
                /gene="LOC113007"
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:2291406"
STS            93574..93657
                /gene="LOC113007"
                /standard_name="STS-F03992"
                /db_xref="UniSTS:33492"
gene            complement(98273..132250)
                /gene="FLJ21799"
                /note="Located on Accession NT_024766"
                /db_xref="LocusID:80011"
mRNA            complement(join(98273..98777,99503..100310,109805..109869,
                112897..113030,118536..118657,119061..119159,
                120013..120154,132107..132250))
                /gene="FLJ21799"
                /product="hypothetical protein FLJ21799"
                /note="Derived by automated computational analysis using
                gene prediction method: BLAST. Supporting evidence
                includes similarity to: 1 mRNA"
                /transcript_id="XM_027756.2"

```

```

/db_xref="GI:18585904"
/db_xref="LocusID:80011"
STS 98315..98465
     /standard_name="RH65278"
     /db_xref="UniSTS:92135"
STS 98352..98512
     /standard_name="SHGC-60612"
     /db_xref="UniSTS:23008"
STS 99413..99618
     /standard_name="RH70729"
     /db_xref="UniSTS:89320"
variation 99457
          /allele="G"
          /allele="T"
          /db_xref="dbSNP:15243"
STS 99977..100167
     /standard_name="RH75360"
     /note="WARNING: map location ambiguous"
     /db_xref="UniSTS:92102"
CDS complement(join(100093..100310,109805..109869,
112897..113030,118536..118657,119061..119159,
120013..120139))
     /gene="FLJ21799"
     /note="Located on Accession NT_024766"
     /codon_start=1
     /protein_id="XP_027756.2"
     /db_xref="GI:18585905"
     /db_xref="LocusID:80011"
STS 100131..100260
     /standard_name="SHGC-33215"
     /note="WARNING: map location ambiguous"
     /db_xref="UniSTS:171029"
variation 104040
          /allele="T"
          /allele="C"
          /db_xref="dbSNP:933716"
variation 113641
          /allele="A"
          /allele="C"
          /db_xref="dbSNP:2895452"
STS 124328..124477
     /standard_name="SHGC-34581"
     /db_xref="UniSTS:33984"
variation 125024
          /allele="A"
          /allele="G"
          /db_xref="dbSNP:767505"
STS 125067..125366
     /standard_name="SHGC-111288"
     /db_xref="UniSTS:182945"
variation 125459..125460
          /allele="-"
          /allele="AT"
          /db_xref="dbSNP:3054322"
variation 125596
          /allele="G"
          /allele="T"
          /db_xref="dbSNP:1833992"
variation 125744
          /allele="A"

```

```

/allele="G"
/db_xref="dbSNP:1423936"
gene      132619..186986
          /gene="LOC89970"
          /note="Located on Accession NT_024766"
          /db_xref="InterimID:89970"
mRNA      join(132619..133336,150661..151165,154215..154267,
          155232..155344,160004..160130,160920..160978,
          163139..163205,163936..164067,167764..167879,
          168304..168447,174374..174485,177743..177845,
          178199..178351,182156..182260,185908..186986)
          /gene="LOC89970"
          /product="similar to hypothetical protein"
          /note="Derived by automated computational analysis using
          gene prediction method: BLAST. Supporting evidence
          includes similarity to: 2 mRNAs"
          /transcript_id="XM_027758.2"
          /db_xref="GI:18585906"
          /db_xref="InterimID:89970"
variation  146137..146138
          /gene="LOC89970"
          /allele="-"
          /allele="TT"
          /db_xref="dbSNP:3055196"
CDS        join(150816..151165,154215..154267,155232..155344,
          160004..160130,160920..160978,163139..163205,
          163936..164067,167764..167879,168304..168447,
          174374..174485,177743..177845,178199..178351,
          182156..182260,185908..186004)
          /gene="LOC89970"
          /note="Located on Accession NT_024766"
          /codon_start=1
          /protein_id="XP_027758.1"
          /db_xref="GI:14778831"
          /db_xref="InterimID:89970"
variation  156205..156206
          /gene="LOC89970"
          /allele="-"
          /allele="CCCT"
          /db_xref="dbSNP:3054336"
variation  156824
          /gene="LOC89970"
          /allele="C"
          /allele="T"
          /db_xref="dbSNP:2399623"
variation  160696
          /gene="LOC89970"
          /allele="G"
          /allele="C"
          /db_xref="dbSNP:918711"
variation  161599
          /gene="LOC89970"
          /allele="G"
          /allele="T"
          /db_xref="dbSNP:715040"
STS        161719..162001
          /gene="LOC89970"
          /standard_name="SHGC-141255"
          /db_xref="UniSTS:182951"
variation  167507

```

```

/ gene="LOC89970"
/ allele="C"
/ allele="T"
variation / db_xref="dbSNP:950003"
170081
/ gene="LOC89970"
/ allele="T"
/ allele="C"
variation / db_xref="dbSNP:958148"
177989
/ gene="LOC89970"
/ allele="T"
/ allele="G"
STS / db_xref="dbSNP:2288006"
187143..187308
/ standard_name="RH68051"
variation / db_xref="UniSTS:14411"
190314
/ allele="A"
/ allele="T"
variation / db_xref="dbSNP:889556"
190866
/ allele="A"
/ allele="C"
/ db_xref="dbSNP:2008317"
gene 192334..200472
/ gene="BART1"
/ note="Located on Accession NT_024766"
/ db_xref="LocusID:23568"
mRNA join(192334..192435,193110..193171,195567..195673,
196797..196882,197441..197537,199196..200472)
/ gene="BART1"
/ product="binder of Arl Two"
/ note="Derived by automated computational analysis using
gene prediction method: BLAST. Supporting evidence
includes similarity to: 1 mRNA"
/ transcript_id="XM_027759.1"
/ db_xref="GI:14778833"
/ db_xref="LocusID:23568"
CDS join(192398..192435,193110..193171,195567..195673,
196797..196882,197441..197537,199196..199297)
/ gene="BART1"
/ note="Located on Accession NT_024766"
/ codon_start=1
/ protein_id="XP_027759.1"
/ db_xref="GI:14778834"
/ db_xref="LocusID:23568"
variation 196203
/ gene="BART1"
/ allele="C"
/ allele="T"
/ db_xref="dbSNP:2046532"
variation 199329
/ gene="BART1"
/ allele="C"
/ allele="T"
/ db_xref="dbSNP:1044196"
variation 199574
/ gene="BART1"
/ allele="A"

```



```

/allele="G"
/db_xref="dbSNP:1044208"
STS 199694..199941
/gene="BART1"
/standard_name="STS-W69175"
/db_xref="UniSTS:8134"
variation 199763
/gene="BART1"
/allele="A"
/allele="G"
/db_xref="dbSNP:1044216"
STS 199807..199956
/gene="BART1"
/standard_name="SHGC-33383"
/db_xref="UniSTS:171030"
variation 200107
/gene="BART1"
/allele="A"
/allele="G"
/db_xref="dbSNP:1044234"
STS 200251..200584
/standard_name="G06868"
/db_xref="UniSTS:2517"
variation 200451
/gene="BART1"
/allele="C"
/allele="A"
/db_xref="dbSNP:14980"
variation 200580
/allele="T"
/allele="G"
/db_xref="dbSNP:14981"
gene complement(203128..210406)
/gene="PMLP"
/note="synonym: PLLP; Located on Accession NT_024766"
/db_xref="LocusID:51090"
/db_xref="MIM:600340"
mRNA complement(join(203128..204059,205494..205616,
208931..209105,210304..210406))
/gene="PMLP"
/product="plasmolipin"
/note="Derived by automated computational analysis using
gene prediction method: BLAST. Supporting evidence
includes similarity to: 2 mRNAs"
/transcript_id="XM_008048.5"
/db_xref="GI:18585907"
/db_xref="LocusID:51090"
/db_xref="MIM:600340"
STS 203164..203391
/standard_name="G06198"
/db_xref="UniSTS:2728"
STS 203164..203294
/standard_name="RH91141"
/db_xref="UniSTS:83897"
STS 203177..203283
/standard_name="D16S3008"
/note="WARNING: map location ambiguous"
/db_xref="UniSTS:154120"
variation 203312
/allele="C"

```

```

/allele="G"
/db_xref="dbSNP:3570"
CDS complement(join(203943..204059,205494..205616,
208931..209105,210304..210356))
/allele="PMLP"
/allele="Located on Accession NT_024766"
/codon_start=1
/protein_id="XP_008048.2"
/db_xref="GI:18585908"
/db_xref="LocusID:51090"
/db_xref="MIM:600340"
variation 208281
/allele="T"
/allele="C"
/db_xref="dbSNP:2081225"
variation 209615..209617
/allele="-"
/allele="TAA"
/db_xref="dbSNP:3054321"
gene complement(220717..270302)
/allele="LOC146471"
/allele="Located on Accession NT_024766"
/db_xref="InterimID:146471"
mRNA complement(join(220717..220783,220942..221025,
221112..221195,222767..222832,223239..223328,
224152..224235,226023..226106,226448..226510,
226702..226791,229921..230004,248354..248437,
249341..249430,250490..250534,252378..252467,
253917..254000,254408..254497,255264..255332,
256133..256201,258698..258787,259799..259882,
261731..261815,262314..262379,264522..264581,
265904..265993,266132..266215,267603..267686,
267833..267916,268970..270302))
/allele="LOC146471"
/product="similar to hypothetical protein FLJ21709 (H. sapiens)"
/allele="Derived by automated computational analysis using gene prediction method: BLAST. Supporting evidence includes similarity to: 1 mRNA"
/transcript_id="XM_085480.1"
/db_xref="GI:18585909"
/db_xref="InterimID:146471"
variation 223806
/allele="G"
/allele="A"
/db_xref="dbSNP:1627144"
variation 226324
/allele="WARNING: map location ambiguous"
/allele="G"
/allele="T"
/db_xref="dbSNP:1167512"
variation 227310
/allele="WARNING: map location ambiguous"
/allele="A"
/allele="G"
/db_xref="dbSNP:1549671"
variation 229907
/allele="WARNING: map location ambiguous"
/allele="C"
/allele="A"

```

variation /db_xref="dbSNP:821469"
231201
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
variation /db_xref="dbSNP:861966"
233167
/allele="C"
/allele="G"
variation /db_xref="dbSNP:1183247"
233996
/note="WARNING: map location ambiguous"
/allele="G"
/allele="T"
variation /db_xref="dbSNP:1167512"
234982
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
variation /db_xref="dbSNP:1549671"
238779
/allele="T"
/allele="C"
variation /db_xref="dbSNP:1183256"
238801
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
variation /db_xref="dbSNP:1184541"
238825
/note="WARNING: map location ambiguous"
/allele="T"
/allele="G"
variation /db_xref="dbSNP:1184540"
238832
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
variation /db_xref="dbSNP:1167744"
238842
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
variation /db_xref="dbSNP:1183823"
238863
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
variation /db_xref="dbSNP:1167743"
239265
/note="WARNING: map location ambiguous"
/allele="G"
/allele="C"
variation /db_xref="dbSNP:1167742"
239335
/note="WARNING: map location ambiguous"
/allele="A"
/allele="C"
variation /db_xref="dbSNP:2052880"
239397

variation /note="WARNING: map location ambiguous"
 /allele="G"
 /allele="A"
 /db_xref="dbSNP:864749"
240353

variation /note="WARNING: map location ambiguous"
 /allele="G"
 /allele="C"
 /db_xref="dbSNP:821471"
244347

variation /note="WARNING: map location ambiguous"
 /allele="C"
 /allele="A"
 /db_xref="dbSNP:821469"
245641

variation /note="WARNING: map location ambiguous"
 /allele="T"
 /allele="C"
 /db_xref="dbSNP:861966"
247261

variation /allele="C"
 /allele="T"
 /db_xref="dbSNP:289725"
247854

variation /allele="T"
 /allele="G"
 /db_xref="dbSNP:185986"
248867

variation /allele="A"
 /allele="C"
 /db_xref="dbSNP:289724"
249366

variation /allele="G"
 /allele="T"
 /db_xref="dbSNP:289723"
252313

variation /allele="A"
 /allele="G"
 /db_xref="dbSNP:2399595"
252371

variation /allele="C"
 /allele="T"
 /db_xref="dbSNP:2399596"
252918

variation /allele="G"
 /allele="A"
 /db_xref="dbSNP:289728"
253197

variation /allele="A"
 /allele="G"
 /db_xref="dbSNP:158483"
253779

variation /allele="C"
 /allele="A"
 /db_xref="dbSNP:158482"
253876

variation /allele="C"
 /allele="A"
 /db_xref="dbSNP:919377"
254113

```

variation      /allele="G"
                /allele="A"
                /db_xref="dbSNP:289727"
                254641
                /allele="G"
                /allele="T"
                /db_xref="dbSNP:158481"
variation      255443
                /allele="A"
                /allele="G"
                /db_xref="dbSNP:289726"
variation      256211
                /allele="C"
                /allele="G"
                /db_xref="dbSNP:864750"
variation      258245
                /allele="G"
                /allele="T"
                /db_xref="dbSNP:1651672"
variation      258446
                /allele="A"
                /allele="G"
                /db_xref="dbSNP:1651671"
variation      258519
                /allele="A"
                /allele="G"
                /db_xref="dbSNP:1672866"
variation      258559
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:1651670"
variation      258662
                /allele="G"
                /allele="C"
                /db_xref="dbSNP:1684580"
variation      258780
                /allele="C"
                /allele="T"
                /db_xref="dbSNP:1672867"
variation      258781
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:1684579"
variation      259216
                /allele="G"
                /allele="C"
                /db_xref="dbSNP:1651669"
variation      259729
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:1651668"
CDS            complement(join(259856..259882,261731..261815,
                262314..262379,264522..264581,265904..265993,
                266132..266215,267603..267686,267833..267916,
                268970..269466))
                /gene="LOC146471"
                /note="Located on Accession NT_024766"
                /codon_start=1
                /protein_id="XP_085480.1"
                /db_xref="GI:18585910"

```

variation	/db_xref="InterimID:146471" 260244 /allele="C" /allele="A"
variation	/db_xref="dbSNP:1684578" 260741 /allele="A" /allele="G"
variation	/db_xref="dbSNP:1672868" 260961 /allele="C" /allele="A"
variation	/db_xref="dbSNP:1684577" 261208 /allele="A" /allele="T"
variation	/db_xref="dbSNP:1428850" 264341 /allele="G" /allele="A"
variation	/db_xref="dbSNP:289754" 267529 /allele="G" /allele="C"
variation	/db_xref="dbSNP:173542" 267628 /allele="G" /allele="C"
variation	/db_xref="dbSNP:190325" 267723 /allele="T" /allele="A"
variation	/db_xref="dbSNP:1684576" 268685 /allele="T" /allele="C"
variation	/db_xref="dbSNP:291039" 268711 /allele="G" /allele="A"
variation	/db_xref="dbSNP:291040" 270914 /allele="G" /allele="T"
variation	/db_xref="dbSNP:1549669" 271211 /allele="C" /allele="G"
variation	/db_xref="dbSNP:1549670" 271319 /allele="T" /allele="C"
variation	/db_xref="dbSNP:821470" 272247 /allele="T" /allele="C"
variation	/db_xref="dbSNP:1672865" 272282 /allele="C" /allele="A"

variation /db_xref="dbSNP:1684575"
272469
/allele="G"
/allele="A"
variation /db_xref="dbSNP:1684574"
273018
/allele="T"
/allele="C"
variation /db_xref="dbSNP:1684573"
273292
/allele="T"
/allele="C"
variation /db_xref="dbSNP:1651667"
273393
/allele="G"
/allele="A"
variation /db_xref="dbSNP:1651666"
273438
/allele="T"
/allele="G"
variation /db_xref="dbSNP:1651665"
274187
/allele="G"
/allele="T"
variation /db_xref="dbSNP:891140"
275395
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
variation /db_xref="dbSNP:1184541"
275419
/note="WARNING: map location ambiguous"
/allele="T"
/allele="G"
variation /db_xref="dbSNP:1184540"
275426
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
variation /db_xref="dbSNP:1167744"
275436
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
variation /db_xref="dbSNP:1183823"
275457
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
variation /db_xref="dbSNP:1167743"
275859
/note="WARNING: map location ambiguous"
/allele="G"
/allele="C"
variation /db_xref="dbSNP:1167742"
275929
/note="WARNING: map location ambiguous"
/allele="A"
/allele="C"
/db_xref="dbSNP:2052880"

variation 275991
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:864749"

variation 276947
/note="WARNING: map location ambiguous"
/allele="G"
/allele="C"
/db_xref="dbSNP:821471"

variation 279631
/allele="G"
/allele="A"
/db_xref="dbSNP:1167741"

variation 281273
/allele="G"
/allele="C"
/db_xref="dbSNP:289702"

variation 281826
/allele="G"
/allele="A"
/db_xref="dbSNP:289703"

variation 282531
/allele="T"
/allele="A"
/db_xref="dbSNP:289704"

variation 282671
/allele="G"
/allele="A"
/db_xref="dbSNP:289705"

variation 282842
/allele="G"
/allele="A"
/db_xref="dbSNP:289706"

variation 284188
/allele="T"
/allele="C"
/db_xref="dbSNP:1151265"

variation 284323
/allele="T"
/allele="C"
/db_xref="dbSNP:1167514"

variation 284784
/allele="G"
/allele="A"
/db_xref="dbSNP:1167513"

variation 285033
/allele="G"
/allele="C"
/db_xref="dbSNP:1672862"

variation 285034
/allele="C"
/allele="A"
/db_xref="dbSNP:1672861"

variation 285127
/allele="T"
/allele="A"
/db_xref="dbSNP:1151264"

variation 285365
/allele="G"

	/allele="A"
	/db_xref="dbSNP:1151263"
variation	286418
	/allele="T"
	/allele="G"
	/db_xref="dbSNP:1618910"
variation	287030
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:1651663"
variation	293150
	/allele="A"
	/allele="T"
	/db_xref="dbSNP:176533"
variation	293528
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:821463"
variation	294133
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:289708"
variation	294392
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:289707"
variation	295657
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:176532"
variation	295938
	/allele="C"
	/allele="G"
	/db_xref="dbSNP:821465"
variation	296921
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:821466"
variation	297650
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:1991515"
variation	298180
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:1875235"
variation	298599
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:1875236"
variation	298688
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:291042"
variation	300153
	/allele="G"
	/allele="T"
	/db_xref="dbSNP:289737"
variation	301085
	/allele="A"

variation /allele="G"
/db_xref="dbSNP:289736"
302733

variation /allele="A"
/allele="G"
/db_xref="dbSNP:289735"
302775

variation /allele="G"
/allele="A"
/db_xref="dbSNP:1864166"
302940

variation /allele="T"
/allele="C"
/db_xref="dbSNP:289734"
305250

variation /allele="A"
/allele="G"
/db_xref="dbSNP:289753"
305358

variation /allele="C"
/allele="T"
/db_xref="dbSNP:289752"
305519

variation /allele="C"
/allele="T"
/db_xref="dbSNP:289751"
305530

variation /allele="A"
/allele="G"
/db_xref="dbSNP:289750"
306000

variation /allele="C"
/allele="T"
/db_xref="dbSNP:289749"
307231

variation /allele="C"
/allele="T"
/db_xref="dbSNP:289748"
307632

variation /allele="A"
/allele="G"
/db_xref="dbSNP:1566439"
308356

variation /allele="A"
/allele="G"
/db_xref="dbSNP:289747"
309545

variation /allele="G"
/allele="A"
/db_xref="dbSNP:172337"
312089

variation /allele="A"
/allele="G"
/db_xref="dbSNP:289746"
312762

variation /allele="G"
/allele="T"
/db_xref="dbSNP:289745"
314192

variation /allele="A"

```

variation    /allele="C"
             /db_xref="dbSNP:289744"
             314498
             /allele="C"
             /allele="T"
             /db_xref="dbSNP:289743"
variation    314532
             /allele="C"
             /allele="G"
             /db_xref="dbSNP:289742"
gene         complement(314538..336537)
             /gene="CETP"
             /note="Located on Accession NT_024766"
             /db_xref="LocusID:1071"
             /db_xref="MIM:118470"
mRNA         complement(join(314538..314790,314971..315056,
316145..316217,316702..316735,317157..317224,
320127..320291,323231..323281,324872..325051,
326299..326390,327001..327061,327280..327349,
328381..328468,328701..328771,328862..328996,
335263..335377,336290..336537))
             /gene="CETP"
             /product="cholesteryl ester transfer protein, plasma"
             /note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BLAST. Supporting evidence includes similarity to:
3 mRNAs"
             /transcript_id="NM_000078.1"
             /db_xref="GI:4557442"
             /db_xref="LocusID:1071"
             /db_xref="MIM:118470"
STS          314538..314714
             /standard_name="D16S3244"
             /db_xref="UniSTS:16234"
STS          314547..314728
             /standard_name="STS-M30185"
             /db_xref="UniSTS:44543"
variation    314632
             /allele="T"
             /allele="C"
             /db_xref="dbSNP:1801706"
CDS          complement(join(314716..314790,314971..315056,
316145..316217,316702..316735,317157..317224,
320127..320291,323231..323281,324872..325051,
326299..326390,327001..327061,327280..327349,
328381..328468,328701..328771,328862..328996,
335263..335377,336290..336407))
             /gene="CETP"
             /note="unclassified translation discrepancy"
             /codon_start=1
             /product="cholesteryl ester transfer protein, plasma
precursor"
             /protein_id="NP_000069.1"
             /db_xref="GI:4557443"
             /db_xref="LocusID:1071"
             /db_xref="MIM:118470"
variation    314742
             /allele="T"
             /allele="C"
             /db_xref="dbSNP:5887"

```

variation 314820
/allele="T"
/allele="C"
/db_xref="dbSNP:289741"

variation 314975
/allele="T"
/allele="C"
/db_xref="dbSNP:1800777"

variation 315002
/allele="T"
/allele="C"
/db_xref="dbSNP:2303790"

variation 315015
/allele="T"
/allele="C"
/db_xref="dbSNP:2228667"

variation 315344
/allele="A"
/allele="G"
/db_xref="dbSNP:289740"

variation 315863
/allele="A"
/allele="T"
/db_xref="dbSNP:289739"

variation 316167
/allele="T"
/allele="C"
/db_xref="dbSNP:5886"

variation 316202
/allele="T"
/allele="C"
/db_xref="dbSNP:5882"

variation 316749
/allele="G"
/allele="A"
/db_xref="dbSNP:1800774"

variation 317203
/allele="G"
/allele="C"
/db_xref="dbSNP:5880"

variation 319595
/allele="C"
/allele="T"
/db_xref="dbSNP:291043"

variation 320282
/allele="T"
/allele="C"
/db_xref="dbSNP:5881"

variation 320358
/allele="G"
/allele="A"
/db_xref="dbSNP:891144"

variation 320842
/allele="C"
/allele="T"
/db_xref="dbSNP:291044"

variation 321346
/allele="A"
/allele="C"
/db_xref="dbSNP:1968905"

variation 322309
/allele="G"
/allele="A"
/db_xref="dbSNP:2033254"

variation 322353
/allele="A"
/allele="G"
/db_xref="dbSNP:289719"

variation 322362
/allele="A"
/allele="G"
/db_xref="dbSNP:289718"

variation 322525
/allele="T"
/allele="A"
/db_xref="dbSNP:736274"

variation 322906
/allele="C"
/allele="T"
/db_xref="dbSNP:289717"

variation 322918
/allele="A"
/allele="T"
/db_xref="dbSNP:289716"

variation 323099
/allele="C"
/allele="A"
/db_xref="dbSNP:2303789"

variation 323786
/allele="A"
/allele="T"
/db_xref="dbSNP:289715"

variation 324007
/allele="T"
/allele="C"
/db_xref="dbSNP:158617"

variation 324067
/allele="C"
/allele="T"
/db_xref="dbSNP:158480"

variation 324246
/allele="C"
/allele="T"
/db_xref="dbSNP:158479"

variation 324560
/allele="G"
/allele="T"
/db_xref="dbSNP:158478"

variation 324684
/allele="C"
/allele="T"
/db_xref="dbSNP:158477"

variation 324843
/allele="C"
/allele="T"
/db_xref="dbSNP:289714"

variation 324941
/allele="G"
/allele="A"
/db_xref="dbSNP:5883"

variation	325465 /allele="A" /allele="T" /db_xref="dbSNP:289713"
variation	325989 /allele="A" /allele="G" /db_xref="dbSNP:289712"
variation	326815 /allele="G" /allele="T" /db_xref="dbSNP:1532624"
variation	326993 /allele="A" /allele="G" /db_xref="dbSNP:1532625"
variation	327023 /allele="G" /allele="A" /db_xref="dbSNP:5885"
variation	328314 /allele="G" /allele="A" /db_xref="dbSNP:891143"
variation	328317 /allele="G" /allele="A" /db_xref="dbSNP:891142"
variation	328571 /allele="C" /allele="A" /db_xref="dbSNP:891141"
variation	332014 /allele="C" /allele="T" /db_xref="dbSNP:820299"
variation	332224 /allele="G" /allele="A" /db_xref="dbSNP:1864165"
variation	332349 /allele="C" /allele="T" /db_xref="dbSNP:708273"
variation	332489 /allele="G" /allele="A" /db_xref="dbSNP:1864164"
variation	335066 /allele="T" /allele="C" /db_xref="dbSNP:1864163"
variation	336011 /allele="C" /allele="T" /db_xref="dbSNP:708272"
variation	336088 /allele="T" /allele="C" /db_xref="dbSNP:711752"

variation 336232
/allele="T"
/allele="C"
/db_xref="dbSNP:2304475"

variation 336342
/allele="T"
/allele="G"
/db_xref="dbSNP:5884"

variation 337064
/allele="T"
/allele="G"
/db_xref="dbSNP:1800775"

variation 337065
/allele="T"
/allele="G"
/db_xref="dbSNP:1799851"

variation 337066
/allele="T"
/allele="G"
/db_xref="dbSNP:1800776"

variation 338391
/allele="G"
/allele="T"
/db_xref="dbSNP:711751"

variation 338422
/allele="C"
/allele="T"
/db_xref="dbSNP:821840"

variation 338432
/allele="C"
/allele="T"
/db_xref="dbSNP:821841"

variation 339458
/allele="C"
/allele="A"
/db_xref="dbSNP:2115429"

variation 340937
/allele="G"
/allele="A"
/db_xref="dbSNP:183130"

variation 341472
/allele="T"
/allele="C"
/db_xref="dbSNP:247619"

variation 341496
/allele="T"
/allele="C"
/db_xref="dbSNP:247618"

variation 341583
/allele="T"
/allele="G"
/db_xref="dbSNP:247617"

variation 342709
/allele="G"
/allele="A"
/db_xref="dbSNP:247616"

variation 343796
/allele="C"
/allele="T"
/db_xref="dbSNP:2399597"

```

variation      344254
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:173539"
variation      347143
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:193695"
variation      347536
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:247615"
variation      348312
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:247614"
variation      349460
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:247613"
variation      349480
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:247612"
variation      349750
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:193694"
variation      350000
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:173538"
variation      350418
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:166017"
STS            351056..351193
                /standard_name="D16S2814"
                /db_xref="UniSTS:153384"
variation      351060
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:247611"
variation      351392
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:173537"
variation      352717
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:1436425"
variation      352718
                /allele="A"
                /allele="G"
                /db_xref="dbSNP:1500299"
variation      352801
                /allele="A"
                /allele="T"
                /db_xref="dbSNP:861884"
variation      354346

```



```

variation    /allele="A"
             /allele="G"
             /db_xref="dbSNP:866038"
354400
             /allele="T"
             /allele="C"
             /db_xref="dbSNP:2518054"
gene        complement(354505..368880)
             /gene="HERPUD1"
             /note="synonyms: SUP, HERP, MIF1, KIAA0025; Located on
             Accession NT_024766"
             /db_xref="LocusID:9709"
mRNA        complement(join(354505..355260,356149..356254,
360778..361128,361664..361786,364205..364335,
365547..365621,365710..365787,368639..368880))
             /gene="HERPUD1"
             /product="homocysteine-inducible, endoplasmic reticulum
             stress-inducible, ubiquitin-like domain member 1"
             /note="unclassified transcription discrepancy; Derived by
             automated computational analysis using gene prediction
             method: BLAST. Supporting evidence includes similarity to:
             1 mRNA"
             /transcript_id="NM_014685.1"
             /db_xref="GI:7661869"
             /db_xref="LocusID:9709"
variation    354618
             /allele="A"
             /allele="G"
             /db_xref="dbSNP:2291955"
variation    354642
             /allele="G"
             /allele="A"
             /db_xref="dbSNP:15104"
STS         354713..354911
             /standard_name="SHGC-61031"
             /db_xref="UniSTS:6122"
variation    354724
             /allele="T"
             /allele="G"
             /db_xref="dbSNP:9497"
variation    354730
             /allele="G"
             /allele="A"
             /db_xref="dbSNP:1802311"
STS         354923..355092
             /standard_name="D16S3200"
             /db_xref="UniSTS:76071"
STS         354924..355070
             /standard_name="RH25263"
             /db_xref="UniSTS:89571"
CDS         complement(join(355096..355260,356149..356254,
360778..361128,361664..361786,364205..364335,
365547..365621,365710..365787,368639..368785))
             /gene="HERPUD1"
             /note="similar to Homo sapiens KIA0025 product encoded by
             GenBank Accession Number D14695; unclassified translation
             discrepancy; KIAA0025 gene product; MMS-inducible gene"
             /codon_start=1
             /evidence=not_experimental
             /product="homocysteine-inducible, endoplasmic reticulum

```

stress-inducible, ubiquitin-like domain member 1"
/protein_id="NP_055500.1"
/db_xref="GI:7661870"
/db_xref="LocusID:9709"
variation 355554
/allele="T"
/allele="C"
/db_xref="dbSNP:881598"
variation 357024
/allele="G"
/allele="T"
/db_xref="dbSNP:952439"
variation 357196
/allele="C"
/allele="T"
/db_xref="dbSNP:952440"
variation 361474
/allele="C"
/allele="T"
/db_xref="dbSNP:247609"
variation 361600
/allele="T"
/allele="C"
/db_xref="dbSNP:2133783"
variation 361886
/allele="G"
/allele="A"
/db_xref="dbSNP:2270835"
variation 362222
/allele="C"
/allele="T"
/db_xref="dbSNP:2562126"
variation 362589
/allele="A"
/allele="C"
/db_xref="dbSNP:247610"
variation 365080
/allele="C"
/allele="T"
/db_xref="dbSNP:1428847"
variation 365251
/allele="A"
/allele="G"
/db_xref="dbSNP:39718"
variation 365786
/allele="C"
/allele="T"
/db_xref="dbSNP:2217332"
variation 366045
/allele="C"
/allele="T"
/db_xref="dbSNP:1820787"
variation 366207
/allele="C"
/allele="T"
/db_xref="dbSNP:1820788"
variation 366835
/allele="A"
/allele="T"
/db_xref="dbSNP:37023"

```

variation      368388
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:2518058"
variation      368401
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:2518057"
variation      368871
                /allele="A"
                /allele="C"
                /db_xref="dbSNP:37024"
variation      368931
                /allele="C"
                /allele="T"
                /db_xref="dbSNP:37025"
variation      370223
                /allele="C"
                /allele="T"
                /db_xref="dbSNP:1366544"
variation      373323
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:190324"
variation      374296
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:193693"
variation      375261
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:247606"
variation      375477
                /allele="G"
                /allele="C"
                /db_xref="dbSNP:2562127"
variation      377666
                /allele="T"
                /allele="G"
                /db_xref="dbSNP:863706"
STS            379428..379703
                /standard_name="D16S673"
                /db_xref="UniSTS:149120"
variation      385183
                /allele="C"
                /allele="T"
                /db_xref="dbSNP:28168"
variation      385816
                /allele="A"
                /allele="G"
                /db_xref="dbSNP:718620"
variation      386325
                /allele="A"
                /allele="G"
                /db_xref="dbSNP:37026"
variation      386431
                /allele="C"
                /allele="G"
                /db_xref="dbSNP:37027"
variation      386495

```

```

variation      /allele="C"
                /allele="G"
                /db_xref="dbSNP:37028"
                387291
variation      /allele="C"
                /allele="T"
                /db_xref="dbSNP:37029"
                388211
variation      /allele="A"
                /allele="G"
                /db_xref="dbSNP:37030"
                388367
variation      /allele="T"
                /allele="C"
                /db_xref="dbSNP:5809"
                388478
variation      /allele="C"
                /allele="G"
                /db_xref="dbSNP:5808"
                388738
variation      /allele="A"
                /allele="G"
                /db_xref="dbSNP:37031"
                388937
variation      /allele="C"
                /allele="T"
                /db_xref="dbSNP:5805"
                388946..389142
STS            /standard_name="STS-X91220"
                /db_xref="UniSTS:10160"
gene           complement(389110..438428)
                /gene="SLC12A3"
                /note="synonyms: TSC, NCCT; Located on Accession
                NT_024766"
                /db_xref="LocusID:6559"
                /db_xref="MIM:600968"
mRNA           complement(join(389110..389283,398084..398151,
                400038..400173,402930..403016,407906..408017,
                409494..409595,410388..410465,412192..412275,
                414518..414624,415456..415596,416079..416190,
                417190..417289,418351..418506,420058..420159,
                422302..422425,422906..423013,423328..423482,
                424394..424478,430872..431002,431196..431307,
                432922..433032,433423..433562,433834..433929,
                435286..435361,436442..436588,438141..438428))
                /gene="SLC12A3"
                /product="solute carrier family 12 (sodium/chloride
                transporters), member 3"
                /note="Derived by automated computational analysis using
                gene prediction method: BLAST. Supporting evidence
                includes similarity to: 1 mRNA"
                /transcript_id="XM_027753.1"
                /db_xref="GI:14778804"
                /db_xref="LocusID:6559"
                /db_xref="MIM:600968"
variation      389124
                /allele="C"
                /allele="G"
                /db_xref="dbSNP:2289112"
variation      389184

```

variation /allele="A"
/allele="G"
/db_xref="dbSNP:2289113"
389655
/allele="A"
/allele="G"
/db_xref="dbSNP:711746"
variation 389812
/allele="C"
/allele="G"
/db_xref="dbSNP:711747"
variation 389865
/allele="C"
/allele="G"
/db_xref="dbSNP:711748"
variation 390038
/allele="A"
/allele="G"
/db_xref="dbSNP:711749"
variation 390075
/allele="A"
/allele="G"
/db_xref="dbSNP:708270"
variation 390262
/allele="T"
/allele="C"
/db_xref="dbSNP:2399594"
variation 390387
/allele="G"
/allele="A"
/db_xref="dbSNP:955513"
variation 390434
/allele="A"
/allele="G"
/db_xref="dbSNP:1366549"
variation 390501
/allele="G"
/allele="A"
/db_xref="dbSNP:957042"
variation 390704
/allele="C"
/allele="A"
/db_xref="dbSNP:955512"
variation 390919
/allele="C"
/allele="T"
/db_xref="dbSNP:2010501"
variation 391671
/allele="G"
/allele="A"
/db_xref="dbSNP:2099107"
variation 391731
/allele="A"
/allele="G"
/db_xref="dbSNP:891139"
variation 393982
/allele="C"
/allele="T"
/db_xref="dbSNP:711750"
gene complement (397705..400324)

```

/ gene="LOC146472"
/ note="Located on Accession NT_024766"
/ db_xref="InterimID:146472"
mRNA complement(join(397705..398151,400038..400324))
/ gene="LOC146472"
/ product="similar to THIAZIDE-SENSITIVE SODIUM-CHLORIDE
COTRANSPORTER (NA-CL SYMPORTER)"
/ note="Derived by automated computational analysis using
gene prediction method: BLAST."
/ transcript_id="XM_085482.1"
/ db_xref="GI:18585911"
/ db_xref="InterimID:146472"
variation 397936
/ allele="A"
/ allele="G"
/ db_xref="dbSNP:2289114"
variation 398071
/ allele="A"
/ allele="G"
/ db_xref="dbSNP:2289115"
CDS complement(join(398080..398151,400038..400292))
/ gene="LOC146472"
/ note="Located on Accession NT_024766"
/ codon_start=1
/ protein_id="XP_085482.1"
/ db_xref="GI:18585912"
/ db_xref="InterimID:146472"
variation 398168
/ allele="C"
/ allele="T"
/ db_xref="dbSNP:2289116"
variation 400000
/ allele="C"
/ allele="T"
/ db_xref="dbSNP:2289117"
variation 402723
/ allele="A"
/ allele="G"
/ db_xref="dbSNP:2304481"
variation 407785
/ allele="G"
/ allele="T"
/ db_xref="dbSNP:2289118"
variation 407941
/ allele="G"
/ allele="A"
/ db_xref="dbSNP:5804"
variation 409632
/ allele="A"
/ allele="G"
/ db_xref="dbSNP:2278489"
variation 409667
/ allele="A"
/ allele="G"
/ db_xref="dbSNP:2278490"
variation 410566
/ allele="A"
/ allele="G"
/ db_xref="dbSNP:2304482"
CDS complement(join(412272..412275,414518..414624,

```

```

415456..415596,416079..416190,417190..417289,
418351..418506,420058..420159,422302..422425,
422906..423013,423328..423482,424394..424478,
430872..431002,431196..431307,432922..433032,
433423..433562,433834..433929,435286..435361,
436442..436588,438141..438422))
/gene="SLC12A3"
/note="Located on Accession NT_024766"
/codon_start=1
/protein_id="XP_027753.1"
/db_xref="GI:14778805"
/db_xref="LocusID:6559"
/db_xref="MIM:600968"
variation 415492
           /allele="G"
           /allele="A"
           /db_xref="dbSNP:5803"
variation 417231
           /allele="T"
           /allele="C"
           /db_xref="dbSNP:5802"
variation 418514
           /allele="A"
           /allele="G"
           /db_xref="dbSNP:2304483"
variation 419009
           /allele="C"
           /allele="G"
           /db_xref="dbSNP:2004916"
variation 422112
           /allele="A"
           /allele="G"
           /db_xref="dbSNP:2304484"
variation 422954
           /allele="G"
           /allele="A"
           /db_xref="dbSNP:5801"
variation 423061
           /allele="A"
           /allele="G"
           /db_xref="dbSNP:2082956"
variation 423564
           /allele="A"
           /allele="G"
           /db_xref="dbSNP:2289119"
variation 424827
           /allele="C"
           /allele="T"
           /db_xref="dbSNP:1865834"
variation 432983
           /allele="G"
           /allele="C"
           /db_xref="dbSNP:1529927"
variation 436282
           /allele="T"
           /allele="A"
           /db_xref="dbSNP:2304480"
variation 436505
           /allele="T"
           /allele="C"

```

```

variation      /db_xref="dbSNP:2304479"
                437470
                /allele="T"
                /allele="C"
variation      /db_xref="dbSNP:1968493"
                438030
                /allele="T"
                /allele="C"
variation      /db_xref="dbSNP:2304478"
                438062
                /allele="C"
                /allele="A"
variation      /db_xref="dbSNP:999662"
                442537
                /allele="C"
                /allele="A"
gene           /db_xref="dbSNP:1436424"
                442848..456794
                /gene="LOC162127"
                /note="Located on Accession NT_024766"
mRNA           /db_xref="InterimID:162127"
                join(442848..443103,453771..453925,456665..456794)
                /gene="LOC162127"
                /product="LOC162127"
                /note="Derived by automated computational analysis using
                gene prediction method: GenomeScan."
                /transcript_id="XM_102420.1"
                /db_xref="GI:18585917"
                /db_xref="InterimID:162127"
CDS            join(443101..443103,453771..453842)
                /gene="LOC162127"
                /note="Located on Accession NT_024766"
                /codon_start=1
                /protein_id="XP_102420.1"
                /db_xref="GI:18585918"
                /db_xref="InterimID:162127"
variation      446671
                /gene="LOC162127"
                /allele="C"
                /allele="A"
variation      /db_xref="dbSNP:1529930"
                452905
                /gene="LOC162127"
                /allele="C"
                /allele="A"
                /db_xref="dbSNP:1865832"
STS           453402..453733
                /gene="LOC162127"
                /standard_name="SHGC-149205"
                /db_xref="UniSTS:176859"
STS           453418..453594
                /gene="LOC162127"
                /standard_name="RH68369"
                /db_xref="UniSTS:41907"
variation      453489
                /gene="LOC162127"
                /allele="G"
                /allele="C"
                /db_xref="dbSNP:735145"
variation      453646

```


	/gene="LOC162127" /allele="T" /allele="C" /db_xref="dbSNP:735144" 456118..456246 /gene="LOC162127" /standard_name="SHGC-37413" /db_xref="UniSTS:30073" 457412 /allele="T" /allele="C" /db_xref="dbSNP:2399562" 458714..458813 /standard_name="SHGC-24014" /db_xref="UniSTS:99865" 458769 /allele="G" /allele="C" /db_xref="dbSNP:1053078" 458893..468916 /gene="LOC146473" /note="Located on Accession NT_024766" /db_xref="InterimID:146473" join(458893..459162,461828..461956,464057..464140, 464592..464709,465935..466055,466946..467062, 468885..468916) /gene="LOC146473" /product="hypothetical gene LOC146473" /note="Derived by automated computational analysis using gene prediction method: BLAST." /transcript_id="XM_097005.1" /db_xref="GI:18585913" /db_xref="InterimID:146473" complement(458897..503174) /gene="KIAA0095" /note="Located on Accession NT_024766" /db_xref="LocusID:9688" complement(join(458897..459162,461828..461956, 464057..464140,464592..464709,465935..466053, 466944..467060,468883..468927,469219..469291, 469407..469533,470255..470446,471273..471356, 472973..473130,474549..474681,479812..479951, 482889..482978,485744..485818,495919..496047, 503110..503174)) /gene="KIAA0095" /product="KIAA0095 gene product" /note="unclassified transcription discrepancy; Derived by automated computational analysis using gene prediction method: BLAST. Supporting evidence includes similarity to: 1 mRNA" /transcript_id="XM_012552.3" /db_xref="GI:14778808" /db_xref="LocusID:9688" complement(join(458897..459162,461828..461956, 464057..464140,464592..464709,465935..466053, 466944..467060,468883..468927,469219..469291, 469407..469533,470255..470446,471273..471356, 472973..473130,474549..474681,479812..479951, 482889..482978,485744..485818,495919..496038)) /gene="KIAA0095"
--	---

```

/feature "note" {
    /text "Located on Accession NT_024766; unclassified translation discrepancy"
}
/feature "codon_start" {
    /start 1
}
/feature "protein_id" {
    /id "XP_012552.3"
}
/feature "db_xref" {
    /db "GI" 14778809
    /db "LocusID" 9688
}
STS
458898..459048
/feature "gene" {
    /name "LOC146473"
}
/feature "standard_name" {
    /name "SHGC-35816"
}
/feature "db_xref" {
    /db "UniSTS" 30835
}
STS
461752..461884
/feature "gene" {
    /name "LOC146473"
}
/feature "standard_name" {
    /name "SHGC-58086"
}
/feature "db_xref" {
    /db "UniSTS" 67904
}
variation
462670
/feature "gene" {
    /name "LOC146473"
}
/feature "allele" {
    /name "G"
}
/feature "allele" {
    /name "A"
}
/feature "db_xref" {
    /db "dbSNP" 1865831
}
variation
462716
/feature "gene" {
    /name "LOC146473"
}
/feature "allele" {
    /name "G"
}
/feature "allele" {
    /name "A"
}
/feature "db_xref" {
    /db "dbSNP" 2007432
}
variation
463376
/feature "gene" {
    /name "LOC146473"
}
/feature "allele" {
    /name "T"
}
/feature "allele" {
    /name "C"
}
/feature "db_xref" {
    /db "dbSNP" 1865830
}
variation
463601
/feature "gene" {
    /name "LOC146473"
}
/feature "allele" {
    /name "T"
}
/feature "allele" {
    /name "C"
}
/feature "db_xref" {
    /db "dbSNP" 1865829
}
variation
463733
/feature "gene" {
    /name "LOC146473"
}
/feature "allele" {
    /name "T"
}
/feature "allele" {
    /name "C"
}
/feature "db_xref" {
    /db "dbSNP" 2304477
}
STS
463919..464247
/feature "gene" {
    /name "LOC146473"
}
/feature "standard_name" {
    /name "SHGC-79844"
}
/feature "db_xref" {
    /db "UniSTS" 101987
}
variation
464078
/feature "gene" {
    /name "LOC146473"
}
/feature "allele" {
    /name "G"
}
/feature "allele" {
    /name "A"
}
/feature "db_xref" {
    /db "dbSNP" 2304476
}
CDS
join(464610..464709,465935..466055,466946..467062,468885..468906)
/feature "gene" {
    /name "LOC146473"
}
/feature "note" {
    /text "Located on Accession NT_024766"
}
/feature "codon_start" {
    /start 1
}
/feature "protein_id" {
    /id "XP_097005.1"
}
/feature "db_xref" {
    /db "GI" 18585914
}
/feature "db_xref" {
    /db "InterimID" 146473
}
variation
468143
/feature "gene" {
    /name "LOC146473"
}
/feature "allele" {
    /name "G"
}
/feature "allele" {
    /name "A"
}

```

variation	/db_xref="dbSNP:1561141" 468873 /gene="LOC146473" /allele="T" /allele="C"
variation	/db_xref="dbSNP:1347591" 471377 /allele="G" /allele="A"
variation	/db_xref="dbSNP:2241770" 473172 /allele="A" /allele="G"
variation	/db_xref="dbSNP:1561140" 475575 /allele="C" /allele="G"
variation	/db_xref="dbSNP:2099536" 480340 /allele="C" /allele="T"
variation	/db_xref="dbSNP:2043634" 480599 /allele="T" /allele="G"
variation	/db_xref="dbSNP:2399560" 480615 /allele="T" /allele="C"
variation	/db_xref="dbSNP:2895432" 482898 /allele="G" /allele="C"
variation	/db_xref="dbSNP:2118017" 485572 /allele="C" /allele="A"
variation	/db_xref="dbSNP:1561139" 486083 /allele="T" /allele="G"
variation	/db_xref="dbSNP:1561138" 488583..488584 /allele="--" /allele="CAGCAG"
variation	/db_xref="dbSNP:3028881" 488898 /allele="T" /allele="C"
variation	/db_xref="dbSNP:1529929" 490465 /allele="T" /allele="G"
variation	/db_xref="dbSNP:1347590" 491124 /allele="T" /allele="C"
variation	/db_xref="dbSNP:1529928" 496024 /allele="G"

http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=nucleotide&list_uids=18... 5/6/2003

AC009090.9:39293..104547,gap(100),AC009090.9:104648..148254,
gap(100),AC009090.9:148355..200925,gap(100),
complement(AC023825.6:10066..14064),
complement(AC020769.4:2434..4129),gap(100),
complement(AC010550.7:11693..17217),gap(100),AC010550.7:3894..6548,
gap(100),AC020769.4:30493..37561,gap(100),AC023825.6:29888..36331,
gap(100),complement(AC010550.7:60152..96861),
complement(AC023825.6:56451..69306),
complement(AC020769.4:20885..22978),gap(100),
complement(AC010550.7:130148..197926),gap(100),
AC012181.6:3490..4927,gap(100),AC012181.6:62709..74434,gap(100),
AC012181.6:146811..202496,gap(100),
complement(AC012181.6:102278..146710),gap(100),
AC012181.6:30176..39123,gap(100),
complement(AC012181.6:50644..62608),gap(100),
AC012181.6:11696..15308,gap(100),
complement(AC012181.6:20285..29985),gap(100),
complement(AC012181.6:39224..50543),gap(100),
AC012181.6:15409..20184,gap(100),AC012181.6:9070..11595,gap(100),
AC012181.6:6313..8969,gap(100),AC012181.6:5028..6212,gap(100),
AC012181.6:2960..3389,gap(100),AC012181.6:1824..2159,gap(100),
AC012181.6:1..1020)

//

[Disclaimer](#) | [Write to the Help Desk](#)
NCBI | NLM | NIH

May 22 2003 16:47:12



[PubMed](#)
[Nucleotide](#)
[Protein](#)
[Genome](#)
[Structure](#)
[PMC](#)
[Taxonomy](#)
[OMIM](#)
[Bio](#)

Search for

☐ 1: NT_015360[gi:18585813] This record was removed as a result of standard genome annotation processing. See the genome build documentation at <http://www.ncbi.nlm.nih.gov/genome/guide/build.html> for further information, or contact info@ncbi.nlm.nih.gov.

LOCUS NT_015360 1074911 bp DNA linear CON 07-FEB-2002
 DEFINITION Homo sapiens chromosome 16 working draft sequence segment.
 ACCESSION NT_015360
 VERSION NT_015360.8 GI:18585813
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1074911)
 AUTHORS NCBI Annotation Project.
 TITLE Direct Submission
 JOURNAL Submitted (06-FEB-2002) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA
 COMMENT GENOME ANNOTATION REFSEQ: NCBI contigs are derived from assembled
 genomic sequence data.
 Also see:
 Documentation of NCBI's Annotation Process

On Feb 7, 2002 this sequence version replaced gi:17487958.
 COMPLETENESS: not full length.

FEATURES Location/Qualifiers
 source 1..1074911
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="16"
 misc_feature 1..193362
 /standard_name="RP11-433P17"
 /note="FISH-mapped clone"
 STS 1125..1239
 /standard_name="D14S779"
 /note="WARNING: map location ambiguous"
 /db_xref="UniSTS:55747"
 variation 3138
 /allele="C"
 /allele="T"
 /db_xref="dbSNP:1218760"
 variation 3273
 /allele="C"
 /allele="T"
 /db_xref="dbSNP:1009429"
 gene 3339..4277
 /gene="OR2C1"

```

      /note="synonym: OLFMF3; Located on Accession NT_015360"
      /db_xref="LocusID:4993"
mRNA 3339..4277
      /gene="OR2C1"
      /product="olfactory receptor, family 2, subfamily C,
member 1"
      /note="Derived by automated computational analysis using
gene prediction method: BLAST,GenomeScan. Supporting
evidence includes similarity to: 1 mRNA"
      /transcript_id="NM_012368.1"
      /db_xref="GI:6912555"
      /db_xref="LocusID:4993"
CDS 3339..4277
      /gene="OR2C1"
      /codon_start=1
      /product="olfactory receptor, family 2, subfamily C,
member 1"
      /protein_id="NP_036500.1"
      /db_xref="GI:6912556"
      /db_xref="LocusID:4993"
variation 3384
      /gene="OR2C1"
      /allele="A"
      /allele="G"
      /db_xref="dbSNP:1218762"
variation 3392
      /gene="OR2C1"
      /allele="A"
      /allele="G"
      /db_xref="dbSNP:1228348"
variation 3785
      /gene="OR2C1"
      /allele="C"
      /allele="G"
      /db_xref="dbSNP:1218763"
variation 5080
      /allele="C"
      /allele="G"
      /db_xref="dbSNP:1230946"
variation 12402
      /allele="A"
      /allele="G"
      /db_xref="dbSNP:1149497"
variation 14162
      /allele="C"
      /allele="G"
      /db_xref="dbSNP:1231070"
gene complement(15469..28060)
      /gene="LOC162103"
      /note="Located on Accession NT_015360"
      /db_xref="InterimID:162103"
mRNA complement(join(15469..15506,15982..16056,16195..16299,
16442..16609,21681..21709,24619..24810,24992..25178,
27958..28060))
      /gene="LOC162103"
      /product="similar to cytochrome c oxidase subunit I"
      /note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
      /transcript_id="XM_091357.1"
      /db_xref="GI:18585799"

```

```

CDS      /db_xref="InterimID:162103"
         complement(join(15469..15506,15982..16056,16195..16299,
         16442..16609,21681..21709,24619..24810,24992..25178,
         27958..28060))
         /gene="LOC162103"
         /note="Located on Accession NT_015360"
         /codon_start=1
         /protein_id="XP_091357.1"
         /db_xref="GI:18585800"
         /db_xref="InterimID:162103"
variation 17924
         /allele="C"
         /allele="T"
         /db_xref="dbSNP:37798"
variation 20004
         /allele="C"
         /allele="G"
         /db_xref="dbSNP:37799"
variation 21048
         /allele="G"
         /allele="T"
         /db_xref="dbSNP:37800"
variation 22725
         /allele="A"
         /allele="G"
         /db_xref="dbSNP:40633"
variation 22924
         /allele="A"
         /allele="G"
         /db_xref="dbSNP:42329"
variation 23516
         /allele="C"
         /allele="T"
         /db_xref="dbSNP:37801"
variation 23588
         /allele="A"
         /allele="G"
         /db_xref="dbSNP:37802"
variation 24317
         /allele="G"
         /allele="T"
         /db_xref="dbSNP:37803"
variation 25460
         /allele="A"
         /allele="G"
         /db_xref="dbSNP:27225"
variation 26482
         /allele="C"
         /allele="T"
         /db_xref="dbSNP:27226"
variation 27180
         /allele="A"
         /allele="G"
         /db_xref="dbSNP:27227"
variation 29335
         /allele="C"
         /allele="T"
         /db_xref="dbSNP:27228"
gene      complement(29488..31064)
         /gene="FLJ20417"

```



```

/feature {
  mRNA {
    /note="Located on Accession NT_015360"
    /db_xref="LocusID:54925"
    complement(29488..31064)
    /gene="FLJ20417"
    /product="hypothetical protein FLJ20417"
    /note="unclassified transcription discrepancy; Derived by
    automated computational analysis using gene prediction
    method: BLAST. Supporting evidence includes similarity to:
    2 mRNAs"
    /transcript_id="NM_017810.1"
    /db_xref="GI:8923385"
    /db_xref="LocusID:54925"
  }
  STS {
    29589..29699
    /standard_name="SHGC-61089"
    /db_xref="UniSTS:25170"
  }
  variation {
    29618
    /allele="T"
    /allele="C"
    /db_xref="dbSNP:7872"
  }
  variation {
    29815
    /allele="C"
    /allele="T"
    /db_xref="dbSNP:27229"
  }
  variation {
    29996
    /allele="T"
    /allele="A"
    /db_xref="dbSNP:1044390"
  }
  CDS {
    complement(30254..30904)
    /gene="FLJ20417"
    /codon_start=1
    /evidence=not_experimental
    /product="hypothetical protein FLJ20417"
    /protein_id="NP_060280.1"
    /db_xref="GI:8923386"
    /db_xref="LocusID:54925"
  }
  variation {
    30951
    /allele="C"
    /allele="T"
    /db_xref="dbSNP:1144623"
  }
  gene {
    complement(31080..48373)
    /gene="MGC4179"
    /note="Located on Accession NT_015360"
    /db_xref="LocusID:79229"
  }
  mRNA {
    complement(join(31080..31113,31861..32343,37410..37533,
    37823..37917,41058..41223,44601..45153,48354..48373))
    /gene="MGC4179"
    /product="hypothetical protein MGC4179"
    /note="unclassified transcription discrepancy; Derived by
    automated computational analysis using gene prediction
    method: BLAST. Supporting evidence includes similarity to:
    1 mRNA"
    /transcript_id="NM_024340.1"
    /db_xref="GI:13236590"
    /db_xref="LocusID:79229"
  }
  STS {
    31263..31389
    /standard_name="SHGC-60797"
    /db_xref="UniSTS:36805"
  }
  variation {
    32101
    /allele="A"
    /allele="G"
  }
}

```

CDS /db_xref="dbSNP:27230"
complement(join(32321..32343,37410..37533,37823..37917,
41058..41223,44601..44963))
/gene="MGC4179"
/note="unclassified translation discrepancy"
/codon_start=1
/product="hypothetical protein MGC4179"
/protein_id="NP_077316.1"
/db_xref="GI:13236591"
/db_xref="LocusID:79229"

variation 32368
 /allele="C"
 /allele="T"
 /db_xref="dbSNP:27231"

variation 34089
 /allele="A"
 /allele="G"
 /db_xref="dbSNP:27728"

variation 34184
 /allele="A"
 /allele="G"
 /db_xref="dbSNP:27232"

variation 34251
 /allele="A"
 /allele="C"
 /db_xref="dbSNP:27233"

variation 35319
 /allele="A"
 /allele="C"
 /db_xref="dbSNP:27234"

variation 36538
 /allele="C"
 /allele="G"
 /db_xref="dbSNP:27235"

variation 36562
 /allele="A"
 /allele="C"
 /db_xref="dbSNP:27236"

variation 37076
 /allele="A"
 /allele="G"
 /db_xref="dbSNP:2074366"

variation 37794
 /allele="A"
 /allele="G"
 /db_xref="dbSNP:27237"

variation 38623
 /allele="A"
 /allele="G"
 /db_xref="dbSNP:27238"

variation 39541
 /allele="C"
 /allele="T"
 /db_xref="dbSNP:27239"

variation 39798
 /allele="A"
 /allele="G"
 /db_xref="dbSNP:1690442"

variation 40603
 /allele="A"

	/allele="T"
	/db_xref="dbSNP:1235850"
variation	40620
	/allele="A"
	/allele="T"
	/db_xref="dbSNP:250455"
variation	40625
	/allele="A"
	/allele="T"
	/db_xref="dbSNP:1234662"
variation	40627
	/allele="A"
	/allele="T"
	/db_xref="dbSNP:250456"
variation	40632
	/allele="A"
	/allele="T"
	/db_xref="dbSNP:1235851"
variation	40633
	/allele="A"
	/allele="T"
	/db_xref="dbSNP:37804"
variation	40657
	/allele="A"
	/allele="T"
	/db_xref="dbSNP:250457"
variation	40671
	/allele="G"
	/allele="T"
	/db_xref="dbSNP:28128"
variation	42648
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:1149492"
variation	43402
	/allele="G"
	/allele="T"
	/db_xref="dbSNP:27240"
variation	44346
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:28089"
variation	44691
	/allele="C"
	/allele="G"
	/db_xref="dbSNP:27241"
variation	46888
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:28603"
variation	48316
	/allele="G"
	/allele="C"
	/db_xref="dbSNP:1878931"
variation	48320
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:1878930"
variation	48510
	/allele="A"

gene /allele="G"
 /db_xref="dbSNP:1230965"
48829..56757
 /gene="ZNF174"
 /note="Located on Accession NT_015360"
 /db_xref="LocusID:7727"
 /db_xref="MIM:603900"
mRNA join(48829..49815,51821..52043,55716..56757)
 /gene="ZNF174"
 /product="zinc finger protein 174"
 /note="unclassified transcription discrepancy; Derived by
 automated computational analysis using gene prediction
 method: BLAST. Supporting evidence includes similarity to:
 1 mRNA"
 /transcript_id="NM_003450.1"
 /db_xref="GI:4508006"
 /db_xref="LocusID:7727"
 /db_xref="MIM:603900"
variation 49290
 /gene="ZNF174"
 /allele="C"
 /allele="T"
 /db_xref="dbSNP:37810"
CDS join(49414..49815,51821..52043,55716..56314)
 /gene="ZNF174"
 /codon_start=1
 /product="zinc finger protein 174"
 /protein_id="NP_003441.1"
 /db_xref="GI:4508007"
 /db_xref="LocusID:7727"
 /db_xref="MIM:603900"
variation 49602
 /gene="ZNF174"
 /allele="G"
 /allele="T"
 /db_xref="dbSNP:37811"
variation 50155
 /gene="ZNF174"
 /allele="A"
 /allele="C"
 /db_xref="dbSNP:1238093"
variation 50173
 /gene="ZNF174"
 /allele="C"
 /allele="T"
 /db_xref="dbSNP:1149491"
variation 50182
 /gene="ZNF174"
 /allele="C"
 /allele="T"
 /db_xref="dbSNP:1690445"
variation 50222
 /gene="ZNF174"
 /allele="C"
 /allele="T"
 /db_xref="dbSNP:1239032"
variation 50268
 /gene="ZNF174"
 /allele="C"
 /allele="T"

variation /db_xref="dbSNP:1149490"
50350
/gene="ZNF174"
/allele="C"
/allele="T"
variation /db_xref="dbSNP:1149489"
50368
/gene="ZNF174"
/allele="A"
/allele="C"
variation /db_xref="dbSNP:1237142"
50399
/gene="ZNF174"
/allele="C"
/allele="T"
variation /db_xref="dbSNP:1236997"
50411
/gene="ZNF174"
/allele="C"
/allele="T"
variation /db_xref="dbSNP:1238751"
50428
/gene="ZNF174"
/allele="A"
/allele="C"
variation /db_xref="dbSNP:1237143"
50458
/gene="ZNF174"
/allele="C"
/allele="T"
variation /db_xref="dbSNP:1230966"
50474
/gene="ZNF174"
/allele="A"
/allele="C"
variation /db_xref="dbSNP:1238385"
50486
/gene="ZNF174"
/allele="A"
/allele="T"
variation /db_xref="dbSNP:1238752"
50525
/gene="ZNF174"
/allele="C"
/allele="T"
variation /db_xref="dbSNP:1237716"
51277
/gene="ZNF174"
/allele="A"
/allele="G"
variation /db_xref="dbSNP:37812"
52474
/gene="ZNF174"
/allele="C"
/allele="T"
variation /db_xref="dbSNP:37813"
52642
/gene="ZNF174"
/allele="C"
/allele="T"

```

variation      /db_xref="dbSNP:37814"
53124
/gene="ZNF174"
/allele="A"
/allele="G"
variation      /db_xref="dbSNP:39729"
53307
/gene="ZNF174"
/allele="A"
/allele="G"
variation      /db_xref="dbSNP:37815"
53766
/gene="ZNF174"
/allele="A"
/allele="G"
variation      /db_xref="dbSNP:37816"
54365
/gene="ZNF174"
/allele="A"
/allele="T"
variation      /db_xref="dbSNP:37817"
54490
/gene="ZNF174"
/allele="A"
/allele="G"
variation      /db_xref="dbSNP:37818"
55614
/gene="ZNF174"
/allele="C"
/allele="T"
STS            /db_xref="dbSNP:37819"
56302..56525
/gene="ZNF174"
/standard_name="STS-U31248"
STS            /db_xref="UniSTS:30862"
56326..56537
/gene="ZNF174"
/standard_name="RH70598"
variation      /db_xref="UniSTS:28276"
56349
/gene="ZNF174"
/allele="A"
/allele="G"
variation      /db_xref="dbSNP:1804582"
56533
/gene="ZNF174"
/allele="A"
/allele="G"
STS            /db_xref="dbSNP:12323"
56604..56731
/gene="ZNF174"
/standard_name="D16S2636"
STS            /db_xref="UniSTS:42437"
56604..56709
/gene="ZNF174"
/standard_name="RH91708"
variation      /db_xref="UniSTS:92722"
57701
/allele="A"
/allele="G"

```

variation /db_xref="dbSNP:250458"
58690
/allele="C"
/allele="T"
variation /db_xref="dbSNP:250459"
59649
/allele="C"
/allele="T"
variation /db_xref="dbSNP:250540"
60603
/allele="C"
/allele="T"
variation /db_xref="dbSNP:250541"
60936
/allele="G"
/allele="T"
variation /db_xref="dbSNP:193935"
61426
/allele="C"
/allele="G"
variation /db_xref="dbSNP:185149"
61911
/allele="C"
/allele="T"
variation /db_xref="dbSNP:250542"
61976
/allele="C"
/allele="T"
variation /db_xref="dbSNP:2641784"
62071
/allele="C"
/allele="T"
variation /db_xref="dbSNP:250543"
62108
/allele="A"
/allele="G"
variation /db_xref="dbSNP:250544"
62413
/allele="C"
/allele="G"
variation /db_xref="dbSNP:2015640"
64220
/note="WARNING: map location ambiguous"
/allele="A"
/allele="C"
variation /db_xref="dbSNP:1690452"
64275
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
variation /db_xref="dbSNP:1714503"
64360
/note="WARNING: map location ambiguous"
/allele="G"
/allele="T"
variation /db_xref="dbSNP:1690453"
64430
/note="WARNING: map location ambiguous"
/allele="C"
/allele="G"

variation	/db_xref="dbSNP:2526287"
	65924
	/allele="C"
	/allele="T"
STS	/db_xref="dbSNP:1230886"
	67901..68078
	/standard_name="D16S475"
	/db_xref="UniSTS:55731"
variation	67989
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:1230887"
	69456
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:250521"
	69480
	/allele="G"
	/allele="T"
variation	/db_xref="dbSNP:250522"
	69505
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:250523"
	69827
	/allele="G"
	/allele="T"
variation	/db_xref="dbSNP:250524"
	72242
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:166101"
	72255
	/allele="G"
	/allele="T"
variation	/db_xref="dbSNP:250537"
	72566
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:1230882"
	73055
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:250535"
	73116
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:250534"
	73918
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:250533"
	74815
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:250532"
	74835
	/allele="C"
	/allele="G"
	/db_xref="dbSNP:250531"

variation	74986 /allele="C" /allele="G" /db_xref="dbSNP:250530"
variation	75084 /allele="A" /allele="T" /db_xref="dbSNP:250529"
variation	76215 /allele="G" /allele="T" /db_xref="dbSNP:250528"
variation	76247 /allele="A" /allele="G" /db_xref="dbSNP:171634"
variation	76604 /allele="C" /allele="T" /db_xref="dbSNP:250527"
variation	76730 /allele="C" /allele="T" /db_xref="dbSNP:166100"
variation	76985 /allele="G" /allele="T" /db_xref="dbSNP:250526"
variation	77072 /allele="C" /allele="G" /db_xref="dbSNP:250525"
variation	77188 /allele="A" /allele="G" /db_xref="dbSNP:2526284"
variation	77192 /allele="C" /allele="T" /db_xref="dbSNP:2526285"
variation	78502 /allele="A" /allele="G" /db_xref="dbSNP:190374"
variation	78697 /allele="A" /allele="G" /db_xref="dbSNP:166099"
variation	78856 /allele="C" /allele="G" /db_xref="dbSNP:37820"
variation	79316 /allele="G" /allele="A" /db_xref="dbSNP:2680235"
variation	79388 /allele="G" /allele="T" /db_xref="dbSNP:185148"

STS 80835..80963
 /standard_name="RH68951"
 /db_xref="UniSTS:24983"
 variation 80861
 /allele="G"
 /allele="A"
 /db_xref="dbSNP:1129568"
 variation 80981..80982
 /allele="-"
 /allele="CT"
 /db_xref="dbSNP:1610892"
 variation 81979
 /allele="C"
 /allele="T"
 /db_xref="dbSNP:37821"
 variation 82423
 /allele="A"
 /allele="G"
 /db_xref="dbSNP:37822"
 variation 82744
 /allele="C"
 /allele="T"
 /db_xref="dbSNP:187507"
 variation 82849
 /allele="A"
 /allele="G"
 /db_xref="dbSNP:37823"
 gene complement(83495..90893)
 /gene="LOC146434"
 /note="Located on Accession NT_015360"
 /db_xref="InterimID:146434"
 mRNA complement(join(83495..84927,88200..88326,90513..90598,
 90752..90893))
 /gene="LOC146434"
 /product="similar to unnamed protein product"
 /note="Derived by automated computational analysis using
 gene prediction method: BLAST. Supporting evidence
 includes similarity to: 1 mRNA"
 /transcript_id="XM_085468.1"
 /db_xref="GI:18585762"
 /db_xref="InterimID:146434"
 variation 83625
 /allele="C"
 /allele="T"
 /db_xref="dbSNP:37824"
 variation 83674
 /allele="A"
 /allele="C"
 /db_xref="dbSNP:12737"
 STS 83699..83884
 /standard_name="RH93596"
 /db_xref="UniSTS:86843"
 CDS complement(join(83813..84927,88200..88326,90513..90545))
 /gene="LOC146434"
 /note="Located on Accession NT_015360"
 /codon_start=1
 /protein_id="XP_085468.1"
 /db_xref="GI:18585763"
 /db_xref="InterimID:146434"
 STS 83931..84075

variation /standard_name="RH69449"
/db_xref="UniSTS:28180"
84590
/allele="A"
/allele="G"
variation /db_xref="dbSNP:2270492"
84945
/allele="A"
/allele="T"
variation /db_xref="dbSNP:40534"
84965
/allele="C"
/allele="T"
variation /db_xref="dbSNP:37825"
85138..85140
/allele="-"
/allele="GAG"
variation /db_xref="dbSNP:2067205"
85727
/allele="C"
/allele="T"
variation /db_xref="dbSNP:37826"
85750
/allele="A"
/allele="G"
variation /db_xref="dbSNP:37827"
85816
/allele="C"
/allele="T"
variation /db_xref="dbSNP:42223"
85962
/allele="A"
/allele="T"
variation /db_xref="dbSNP:37828"
86023
/allele="C"
/allele="T"
variation /db_xref="dbSNP:37829"
87037
/allele="C"
/allele="T"
variation /db_xref="dbSNP:40222"
87738
/allele="A"
/allele="G"
variation /db_xref="dbSNP:37830"
88272
/allele="A"
/allele="T"
variation /db_xref="dbSNP:2270493"
88315
/allele="C"
/allele="G"
variation /db_xref="dbSNP:2270494"
88326
/allele="C"
/allele="T"
variation /db_xref="dbSNP:2270495"
88460
/allele="C"

variation /allele="G"
/db_xref="dbSNP:2270496"
88602

variation /allele="C"
/allele="T"
/db_xref="dbSNP:37831"
88665

variation /allele="C"
/allele="G"
/db_xref="dbSNP:2526286"
88822

variation /allele="A"
/allele="G"
/db_xref="dbSNP:42971"
89108

variation /allele="C"
/allele="T"
/db_xref="dbSNP:41471"
89302

variation /allele="C"
/allele="G"
/db_xref="dbSNP:37832"
90887

variation /allele="A"
/allele="G"
/db_xref="dbSNP:2270497"
91029

variation /allele="G"
/allele="T"
/db_xref="dbSNP:2270498"
91081

variation /allele="C"
/allele="T"
/db_xref="dbSNP:2270499"
91599

variation /allele="A"
/allele="T"
/db_xref="dbSNP:27242"
97431

variation /allele="A"
/allele="G"
/db_xref="dbSNP:37833"
97906

variation /allele="A"
/allele="G"
/db_xref="dbSNP:28810"
98993

variation /allele="C"
/allele="G"
/db_xref="dbSNP:37834"
99045

variation /allele="A"
/allele="G"
/db_xref="dbSNP:37835"
101127

variation /allele="C"
/allele="T"
/db_xref="dbSNP:40223"
102013

variation /allele="C"

	/allele="T"
	/db_xref="dbSNP:37836"
variation	103610
	/allele="C"
	/allele="G"
	/db_xref="dbSNP:40535"
variation	105322
	/allele="G"
	/allele="T"
	/db_xref="dbSNP:1635382"
variation	105989
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:37837"
variation	106429
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:40363"
variation	107038
	/allele="G"
	/allele="T"
	/db_xref="dbSNP:39730"
variation	107127
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:37838"
variation	107683
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:37839"
variation	107789
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:250636"
variation	108380
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:250637"
variation	109269
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:250626"
variation	110084
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:37774"
variation	110223
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:37773"
variation	110232
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:37772"
variation	110255
	/allele="G"
	/allele="T"
	/db_xref="dbSNP:37771"
variation	110748
	/allele="C"

	/allele="G"
	/db_xref="dbSNP:37770"
variation	111970
	/allele="C"
	/allele="G"
	/db_xref="dbSNP:37769"
variation	112167
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:37768"
variation	112231
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:40447"
variation	112352
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:37767"
variation	112668
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:37766"
variation	112743
	/allele="G"
	/allele="C"
	/db_xref="dbSNP:28401"
variation	114970
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:1635392"
variation	115024
	/allele="C"
	/allele="G"
	/db_xref="dbSNP:1690441"
variation	115176
	/allele="C"
	/allele="G"
	/db_xref="dbSNP:1690443"
variation	115739
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:1690444"
variation	116398
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:1690446"
variation	116602
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:1690447"
variation	117694
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:1635393"
variation	117716
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:1635394"
variation	118006
	/allele="A"

```

variation    /allele="G"
              /db_xref="dbSNP:1617722"
              118093
              /allele="C"
              /allele="G"
              /db_xref="dbSNP:1690449"
variation    118254
              /allele="A"
              /allele="G"
              /db_xref="dbSNP:1690450"
variation    118647
              /allele="A"
              /allele="G"
              /db_xref="dbSNP:1690451"
variation    120205
              /note="WARNING: map location ambiguous"
              /allele="C"
              /allele="T"
              /db_xref="dbSNP:250633"
variation    120245
              /note="WARNING: map location ambiguous"
              /allele="T"
              /allele="C"
              /db_xref="dbSNP:250632"
              /db_xref="dbSNP:1690455"
variation    120413
              /note="WARNING: map location ambiguous"
              /allele="C"
              /allele="G"
              /db_xref="dbSNP:250631"
variation    120805
              /note="WARNING: map location ambiguous"
              /allele="C"
              /allele="T"
              /db_xref="dbSNP:166103"
variation    121440
              /note="WARNING: map location ambiguous"
              /allele="C"
              /allele="T"
              /db_xref="dbSNP:250630"
variation    122355
              /note="WARNING: map location ambiguous"
              /allele="G"
              /allele="A"
              /db_xref="dbSNP:2087997"
variation    122632
              /note="WARNING: map location ambiguous"
              /allele="A"
              /allele="C"
              /db_xref="dbSNP:250629"
gene         123007..137720
              /gene="LOC162104"
              /note="Located on Accession NT_015360"
              /db_xref="InterimID:162104"
mRNA         join(123007..123113,123499..123538,127427..127575,
              129208..129247,137520..137720)
              /gene="LOC162104"
              /product="LOC162104"
              /note="Derived by automated computational analysis using
              gene prediction method: GenomeScan."

```

CDS
/transcript_id="XM_102406.1"
/db_xref="GI:18585801"
/db_xref="InterimID:162104"
join(123007..123113,123499..123538,127427..127575,
129208..129247,137520..137720)
/gene="LOC162104"
/note="Located on Accession NT_015360"
/codon_start=1
/protein_id="XP_102406.1"
/db_xref="GI:18585802"
/db_xref="InterimID:162104"

variation
124170
/gene="LOC162104"
/note="WARNING: map location ambiguous"
/allele="A"
/allele="C"
/db_xref="dbSNP:250628"

variation
124251
/gene="LOC162104"
/note="WARNING: map location ambiguous"
/allele="A"
/allele="G"
/db_xref="dbSNP:250627"

variation
125911
/gene="LOC162104"
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
/db_xref="dbSNP:250633"

variation
125956
/gene="LOC162104"
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:250632"
/db_xref="dbSNP:1690455"

variation
126124
/gene="LOC162104"
/note="WARNING: map location ambiguous"
/allele="C"
/allele="G"
/db_xref="dbSNP:250631"

variation
126516
/gene="LOC162104"
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
/db_xref="dbSNP:166103"

variation
127151
/gene="LOC162104"
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
/db_xref="dbSNP:250630"

variation
128063
/gene="LOC162104"
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:2087997"


```

variation      128340
                /gene="LOC162104"
                /note="WARNING: map location ambiguous"
                /allele="A"
                /allele="C"
                /db_xref="dbSNP:250629"
variation      129879
                /gene="LOC162104"
                /note="WARNING: map location ambiguous"
                /allele="A"
                /allele="C"
                /db_xref="dbSNP:250628"
variation      129960
                /gene="LOC162104"
                /note="WARNING: map location ambiguous"
                /allele="A"
                /allele="G"
                /db_xref="dbSNP:250627"
STS            133674..133788
                /gene="LOC162104"
                /standard_name="D14S779"
                /note="WARNING: map location ambiguous"
                /db_xref="UniSTS:55747"
variation      140239
                /note="WARNING: map location ambiguous"
                /allele="A"
                /allele="C"
                /db_xref="dbSNP:1690452"
variation      140294
                /note="WARNING: map location ambiguous"
                /allele="C"
                /allele="T"
                /db_xref="dbSNP:1714503"
variation      140379
                /note="WARNING: map location ambiguous"
                /allele="G"
                /allele="T"
                /db_xref="dbSNP:1690453"
variation      140449
                /note="WARNING: map location ambiguous"
                /allele="C"
                /allele="G"
                /db_xref="dbSNP:2526287"
gene            148268..172606
                /gene="LOC124208"
                /note="Located on Accession NT_015360"
                /db_xref="InterimID:124208"
mRNA           join(148268..148707,148758..148868,172145..172407,
                172503..172606)
                /gene="LOC124208"
                /product="similar to dJ475N16.3 (novel protein similar to
                RPL7A (60S ribosomal protein L7A))"
                /note="Derived by automated computational analysis using
                gene prediction method: GenomeScan."
                /transcript_id="XM_064035.1"
                /db_xref="GI:17487922"
                /db_xref="InterimID:124208"
CDS            join(148268..148707,148758..148868,172145..172407,
                172503..172606)
                /gene="LOC124208"

```

/note="Located on Accession NT_015360"
/codon_start=1
/protein_id="XP_064035.1"
/db_xref="GI:17487923"
/db_xref="InterimID:124208"
variation 153747
/gene="LOC124208"
/allele="G"
/allele="A"
/db_xref="dbSNP:1968055"
variation 154163
/gene="LOC124208"
/allele="C"
/allele="A"
/db_xref="dbSNP:1231090"
variation 154714
/gene="LOC124208"
/allele="T"
/allele="A"
/db_xref="dbSNP:1231089"
variation 155221
/gene="LOC124208"
/allele="G"
/allele="C"
/db_xref="dbSNP:1234664"
variation 155617
/gene="LOC124208"
/allele="G"
/allele="A"
/db_xref="dbSNP:1231088"
variation 155707
/gene="LOC124208"
/allele="G"
/allele="A"
/db_xref="dbSNP:1231087"
variation 155817
/gene="LOC124208"
/allele="T"
/allele="A"
/db_xref="dbSNP:2106862"
variation 156977
/gene="LOC124208"
/allele="T"
/allele="G"
/db_xref="dbSNP:1231099"
variation 158187
/gene="LOC124208"
/allele="T"
/allele="C"
/db_xref="dbSNP:1231098"
variation 159085
/gene="LOC124208"
/allele="G"
/allele="A"
/db_xref="dbSNP:166098"
variation 159149
/gene="LOC124208"
/allele="T"
/allele="C"
/db_xref="dbSNP:1231096"

variation	159365 /gene="LOC124208" /allele="G" /allele="C" /db_xref="dbSNP:1234659"
variation	160886 /gene="LOC124208" /allele="T" /allele="C" /db_xref="dbSNP:250485"
variation	162471 /gene="LOC124208" /allele="T" /allele="A" /db_xref="dbSNP:1231091"
variation	166819 /gene="LOC124208" /allele="G" /allele="A" /db_xref="dbSNP:250470"
variation	167346 /gene="LOC124208" /allele="C" /allele="A" /db_xref="dbSNP:37846"
variation	167454 /gene="LOC124208" /allele="T" /allele="C" /db_xref="dbSNP:37845"
variation	169607 /gene="LOC124208" /allele="T" /allele="C" /db_xref="dbSNP:37844"
variation	169778 /gene="LOC124208" /allele="G" /allele="A" /db_xref="dbSNP:1690429"
variation	169790 /gene="LOC124208" /allele="T" /allele="G" /db_xref="dbSNP:37843"
variation	169841 /gene="LOC124208" /allele="T" /allele="C" /db_xref="dbSNP:190373"
variation	170393 /gene="LOC124208" /allele="T" /allele="C" /db_xref="dbSNP:2360762"
variation	175051 /allele="T" /allele="G" /db_xref="dbSNP:37842"
variation	175677

```

variation    /allele="T"
              /allele="C"
              /db_xref="dbSNP:37841"
              176526
              /allele="G"
              /allele="C"
              /db_xref="dbSNP:2011169"
variation    176649
              /allele="T"
              /allele="C"
              /db_xref="dbSNP:2011029"
variation    176716
              /allele="G"
              /allele="A"
              /db_xref="dbSNP:1963299"
STS          176977..177101
              /standard_name="SHGC-60769"
              /db_xref="UniSTS:33463"
gene         complement(177219..193992)
              /gene="LOC146435"
              /note="Located on Accession NT_015360"
              /db_xref="InterimID:146435"
mRNA         complement(join(177219..178603,178771..178881,
              182618..182744,183025..183116,183845..184040,
              190150..190582,193785..193992))
              /gene="LOC146435"
              /product="similar to unnamed protein product"
              /note="Derived by automated computational analysis using
              gene prediction method: BLAST. Supporting evidence
              includes similarity to: 1 mRNA"
              /transcript_id="XM_085465.1"
              /db_xref="GI:18585764"
              /db_xref="InterimID:146435"
STS          177267..177398
              /standard_name="RH45212"
              /db_xref="UniSTS:90620"
STS          177336..177609
              /standard_name="RH69709"
              /db_xref="UniSTS:27702"
STS          177338..177612
              /standard_name="SHGC-133103"
              /db_xref="UniSTS:171017"
STS          177437..177579
              /standard_name="SHGC-64870"
              /db_xref="UniSTS:52239"
CDS          complement(join(177924..178603,178771..178881,
              182618..182717))
              /gene="LOC146435"
              /note="Located on Accession NT_015360"
              /codon_start=1
              /protein_id="XP_085465.1"
              /db_xref="GI:18585765"
              /db_xref="InterimID:146435"
variation    182840
              /allele="C"
              /allele="A"
              /db_xref="dbSNP:37840"
STS          183535..183694
              /standard_name="RH65204"
              /db_xref="UniSTS:92175"

```

```

variation      183776
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:757108"
variation      183909
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:2240024"
variation      188494
                /allele="C"
                /allele="A"
                /db_xref="dbSNP:1714502"
variation      188959
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:1149483"
variation      190529
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:1149484"
variation      190758
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:1149485"
variation      191891
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:2524313"
variation      191892
                /allele="G"
                /allele="C"
                /db_xref="dbSNP:2680232"
gene           194393..205294
                /gene="LOC91151"
                /note="Located on Accession NT_015360"
                /db_xref="LocusID:91151"
mRNA           join(194393..196690,205243..205294)
                /gene="LOC91151"
                /product="similar to jerky (mouse) homolog-like"
                /note="unclassified transcription discrepancy; Derived by
                automated computational analysis using gene prediction
                method: BLAST. Supporting evidence includes similarity to:
                2 mRNAs"
                /transcript_id="NM_033208.1"
                /db_xref="GI:15082243"
                /db_xref="LocusID:91151"
STS           194397..194546
                /gene="LOC91151"
                /standard_name="SHGC-37723"
                /db_xref="UniSTS:72606"
variation      195107
                /gene="LOC91151"
                /allele="T"
                /allele="G"
                /db_xref="dbSNP:2107216"
CDS           join(195179..196690,205243..205266)
                /gene="LOC91151"
                /note="unclassified translation discrepancy"
                /codon_start=1
                /evidence=not_experimental

```

```

/product="similar to jerky (mouse) homolog-like"
/protein_id="NP_149985.1"
/db_xref="GI:15082244"
/db_xref="LocusID:91151"
STS      196683..196813
         /gene="LOC91151"
         /standard_name="RH92140"
         /db_xref="UniSTS:84932"
variation 197622
         /gene="LOC91151"
         /allele="G"
         /allele="C"
         /db_xref="dbSNP:220377"
variation 198417
         /gene="LOC91151"
         /allele="T"
         /allele="A"
         /db_xref="dbSNP:183389"
variation 198426
         /gene="LOC91151"
         /allele="T"
         /allele="G"
         /db_xref="dbSNP:183388"
variation 199564
         /gene="LOC91151"
         /allele="C"
         /allele="A"
         /db_xref="dbSNP:220382"
variation 201175
         /gene="LOC91151"
         /allele="T"
         /allele="C"
         /db_xref="dbSNP:220381"
variation 201743
         /gene="LOC91151"
         /allele="T"
         /allele="G"
         /db_xref="dbSNP:1149486"
variation 202694
         /gene="LOC91151"
         /allele="G"
         /allele="C"
         /db_xref="dbSNP:1052997"
gene      complement(204336..205570)
         /gene="LOC146436"
         /note="Located on Accession NT_015360"
         /db_xref="InterimID:146436"
mRNA     complement(join(204336..204531,205253..205570))
         /gene="LOC146436"
         /product="similar to FPM315"
         /note="Derived by automated computational analysis using
gene prediction method: BLAST."
         /transcript_id="XM_085469.1"
         /db_xref="GI:18585766"
         /db_xref="InterimID:146436"
gene     complement(204339..212266)
         /gene="ZNF263"
         /note="synonym: FPM315; Located on Accession NT_015360"
         /db_xref="LocusID:10127"
         /db_xref="MIM:604191"

```

mRNA complement(join(204339..206400,207223..207339,209644..209770,210039..210112,210554..210734,211588..212266))
 /gene="ZNF263"
 /product="zinc finger protein 263"
 /note="unclassified transcription discrepancy; Derived by automated computational analysis using gene prediction method: BLAST. Supporting evidence includes similarity to:
 1 mRNA"
 /transcript_id="NM_005741.1"
 /db_xref="GI:5032240"
 /db_xref="LocusID:10127"
 /db_xref="MIM:604191"

variation 204460
 /gene="LOC91151"
 /allele="G"
 /allele="C"
 /db_xref="dbSNP:1059812"

STS 204492..204658
 /gene="LOC91151"
 /standard_name="G19656;A001U12"
 /db_xref="UniSTS:39552"
 /db_xref="UniSTS:39553"

CDS complement(join(204505..204531,205253..205525))
 /gene="LOC146436"
 /note="Located on Accession NT_015360"
 /codon_start=1
 /protein_id="XP_085469.1"
 /db_xref="GI:18585767"
 /db_xref="InterimID:146436"

STS 204528..204666
 /gene="LOC91151"
 /standard_name="D16S2676"
 /db_xref="UniSTS:152425"

variation 204948
 /gene="LOC91151"
 /allele="G"
 /allele="A"
 /db_xref="dbSNP:220380"

variation 205184
 /gene="LOC91151"
 /allele="G"
 /allele="C"
 /db_xref="dbSNP:2074527"

variation 205185
 /gene="LOC91151"
 /allele="T"
 /allele="C"
 /db_xref="dbSNP:2074526"

CDS complement(join(205235..206400,207223..207339,209644..209770,210039..210112,210554..210734,211588..211974))
 /gene="ZNF263"
 /note="unclassified translation discrepancy"
 /codon_start=1
 /product="zinc finger protein 263"
 /protein_id="NP_005732.1"
 /db_xref="GI:5032241"
 /db_xref="LocusID:10127"
 /db_xref="MIM:604191"

```

variation      206358
                /allele="G"
                /allele="C"
                /db_xref="dbSNP:220379"
variation      207450
                /allele="G"
                /allele="C"
                /db_xref="dbSNP:188761"
variation      208533
                /allele="C"
                /allele="T"
                /db_xref="dbSNP:765992"
variation      208558
                /allele="C"
                /allele="T"
                /db_xref="dbSNP:765991"
variation      208575
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:1238097"
variation      208826
                /allele="C"
                /allele="T"
                /db_xref="dbSNP:765993"
variation      209232
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:188760"
variation      212402
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:186371"
variation      212426
                /allele="G"
                /allele="T"
                /db_xref="dbSNP:220378"
gene           complement(212827..222115)
                /gene="LOC146437"
                /note="Located on Accession NT_015360"
                /db_xref="InterimID:146437"
mRNA           complement(join(212827..213079,222078..222115))
                /gene="LOC146437"
                /product="LOC146437"
                /note="Derived by automated computational analysis using
                gene prediction method: GenomeScan."
                /transcript_id="XM_102407.1"
                /db_xref="GI:18585768"
                /db_xref="InterimID:146437"
CDS            complement(join(212827..213079,222078..222115))
                /gene="LOC146437"
                /note="Located on Accession NT_015360"
                /codon_start=1
                /protein_id="XP_102407.1"
                /db_xref="GI:18585769"
                /db_xref="InterimID:146437"
variation      215558
                /allele="T"
                /allele="G"
                /db_xref="dbSNP:170382"
variation      215614

```



```

/allele="G"
/allele="A"
/db_xref="dbSNP:458522"
variation 217275
/allele="C"
/allele="A"
/db_xref="dbSNP:220376"
variation 217951
/allele="G"
/allele="A"
/db_xref="dbSNP:1008289"
variation 219558
/allele="T"
/allele="G"
/db_xref="dbSNP:2524314"
variation 222224
/allele="T"
/allele="C"
/db_xref="dbSNP:190081"
variation 224388
/allele="C"
/allele="G"
/db_xref="dbSNP:2680220"
variation 224445
/allele="T"
/allele="C"
/db_xref="dbSNP:1235951"
variation 226600
/allele="A"
/allele="G"
/db_xref="dbSNP:224243"
variation 227845
/allele="A"
/allele="C"
/db_xref="dbSNP:224242"
variation 228615
/allele="G"
/allele="A"
/db_xref="dbSNP:1149487"
variation 228757
/allele="C"
/allele="T"
/db_xref="dbSNP:224241"
variation 229453
/allele="C"
/allele="T"
/db_xref="dbSNP:224240"
STS 229799..229933
/standard_name="SHGC-58951"
/db_xref="UniSTS:94503"
variation 230470
/allele="A"
/allele="G"
/db_xref="dbSNP:224239"
gene complement(231214..238843)
/gene="LOC162105"
/note="Located on Accession NT_015360"
/db_xref="InterimID:162105"
mRNA complement(join(231214..231882,238823..238843))
/gene="LOC162105"

```

```

/product="LOC162105"
/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_102408.1"
/db_xref="GI:18585803"
/db_xref="InterimID:162105"
CDS complement(231214..231294)
/gene="LOC162105"
/note="Located on Accession NT_015360"
/codon_start=1
/protein_id="XP_102408.1"
/db_xref="GI:18585804"
/db_xref="InterimID:162105"
variation 232768
/allele="G"
/allele="A"
/db_xref="dbSNP:417929"
variation 233462
/allele="G"
/allele="A"
/db_xref="dbSNP:1235939"
variation 234910
/allele="C"
/allele="T"
/db_xref="dbSNP:178618"
variation 235472
/allele="C"
/allele="T"
/db_xref="dbSNP:1228385"
variation 235638
/allele="A"
/allele="G"
/db_xref="dbSNP:1235946"
variation 235814
/allele="A"
/allele="G"
/db_xref="dbSNP:224231"
variation 237436
/allele="T"
/allele="C"
/db_xref="dbSNP:224230"
variation 237627
/allele="G"
/allele="T"
/db_xref="dbSNP:224229"
variation 238074
/allele="C"
/allele="G"
/db_xref="dbSNP:224228"
variation 238227
/allele="C"
/allele="T"
/db_xref="dbSNP:224227"
gene 239166..253765
/gene="MEFV"
/note="synonyms: FMF, MEF, TRIM20; Located on Accession
NT_015360"
/db_xref="LocusID:4210"
/db_xref="MIM:249100"
mRNA join(239166..239482,241003..241635,246013..246362,

```

```

246789..246884,248547..248777,249246..249268,
251205..251320,251507..251539,251901..251933,
252099..253765)
/gene="MEFV"
/product="Mediterranean fever"
/note="Derived by automated computational analysis using
gene prediction method: BLAST. Supporting evidence
includes similarity to: 3 mRNAs"
/transcript_id="XM_007971.3"
/db_xref="GI:13648497"
/db_xref="LocusID:4210"
/db_xref="MIM:249100"
CDS
join(239206..239482,241003..241635,246013..246362,
246789..246884,248547..248777,249246..249268,
251205..251320,251507..251539,251901..251933,
252099..252652)
/gene="MEFV"
/note="Located on Accession NT_015360"
/codon_start=1
/protein_id="XP_007971.3"
/db_xref="GI:13648498"
/db_xref="LocusID:4210"
/db_xref="MIM:249100"
variation
240061
/gene="MEFV"
/allele="A"
/allele="G"
/db_xref="dbSNP:224226"
variation
240453
/gene="MEFV"
/allele="A"
/allele="G"
/db_xref="dbSNP:2550396"
variation
241031
/gene="MEFV"
/allele="C"
/allele="T"
/db_xref="dbSNP:224225"
variation
241034
/gene="MEFV"
/allele="C"
/allele="T"
/db_xref="dbSNP:1801179"
variation
241139
/gene="MEFV"
/allele="A"
/allele="G"
/db_xref="dbSNP:224224"
variation
241220
/gene="MEFV"
/allele="A"
/allele="C"
/db_xref="dbSNP:224223"
variation
241330
/gene="MEFV"
/allele="A"
/allele="G"
/db_xref="dbSNP:224222"
variation
241654
/gene="MEFV"

```

	/allele="A"
	/allele="T"
variation	/db_xref="dbSNP:2735789"
	242262
	/gene="MEFV"
	/allele="A"
	/allele="T"
variation	/db_xref="dbSNP:224221"
	242483
	/gene="MEFV"
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:182674"
	242540
	/gene="MEFV"
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:2550397"
	242558
	/gene="MEFV"
	/allele="C"
	/allele="A"
variation	/db_xref="dbSNP:2741922"
	242994..242995
	/gene="MEFV"
	/allele="-"
	/allele="TT"
variation	/db_xref="dbSNP:3029898"
	243019
	/gene="MEFV"
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:224220"
	243480
	/gene="MEFV"
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:224219"
	243896
	/gene="MEFV"
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:224218"
	244036
	/gene="MEFV"
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:224217"
	244129
	/gene="MEFV"
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:2238408"
	244172
	/gene="MEFV"
	/allele="C"
	/allele="G"
	/allele="T"
variation	/db_xref="dbSNP:224216"
	244433

	/gene="MEFV"
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:224215"
	244443
	/gene="MEFV"
	/allele="T"
	/allele="C"
variation	/db_xref="dbSNP:2238407"
	244497
	/gene="MEFV"
	/allele="G"
	/allele="C"
variation	/db_xref="dbSNP:2238406"
	244634
	/gene="MEFV"
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:2550398"
	244755
	/gene="MEFV"
	/allele="G"
	/allele="T"
variation	/db_xref="dbSNP:2550399"
	245021
	/gene="MEFV"
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:2238405"
	245279
	/gene="MEFV"
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:224214"
	246044
	/gene="MEFV"
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:224213"
	246928
	/gene="MEFV"
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:224212"
	247151
	/gene="MEFV"
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:224211"
	247719
	/gene="MEFV"
	/allele="C"
	/allele="G"
variation	/db_xref="dbSNP:224210"
	247940
	/gene="MEFV"
	/allele="G"
	/allele="T"
variation	/db_xref="dbSNP:224209"
	248612

variation /gene="MEFV"
/allele="A"
/allele="G"
/db_xref="dbSNP:224208"
248618

variation /gene="MEFV"
/allele="A"
/allele="G"
/db_xref="dbSNP:224207"
248720

variation /gene="MEFV"
/allele="C"
/allele="T"
/db_xref="dbSNP:224206"
249177

variation /gene="MEFV"
/allele="A"
/allele="G"
/db_xref="dbSNP:224205"
249364

variation /gene="MEFV"
/allele="C"
/allele="T"
/db_xref="dbSNP:224204"
249454

variation /gene="MEFV"
/allele="G"
/allele="A"
/db_xref="dbSNP:767067"
250079

variation /gene="MEFV"
/allele="A"
/allele="G"
/db_xref="dbSNP:224203"
250399

variation /gene="MEFV"
/allele="A"
/allele="G"
/db_xref="dbSNP:170385"
250408

variation /gene="MEFV"
/allele="A"
/allele="G"
/db_xref="dbSNP:170384"
250557

variation /gene="MEFV"
/allele="A"
/allele="G"
/db_xref="dbSNP:182673"
250574

variation /gene="MEFV"
/allele="A"
/allele="G"
/db_xref="dbSNP:172791"
250727

variation /gene="MEFV"
/allele="A"
/allele="G"
/db_xref="dbSNP:172790"
250862

	/gene="MEFV"
	/allele="G"
	/allele="T"
variation	/db_xref="dbSNP:170383"
	251115
	/gene="MEFV"
	/allele="T"
	/allele="C"
variation	/db_xref="dbSNP:1231124"
	251871
	/gene="MEFV"
	/allele="T"
	/allele="A"
variation	/db_xref="dbSNP:1231123"
	251905
	/gene="MEFV"
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:1231122"
	252424
	/gene="MEFV"
	/allele="A"
	/allele="G"
variation	/db_xref="dbSNP:2234939"
	252785
	/gene="MEFV"
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:2075849"
	252897
	/gene="MEFV"
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:2741919"
	252919
	/gene="MEFV"
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:2741918"
	253395
	/gene="MEFV"
	/allele="C"
	/allele="T"
variation	/db_xref="dbSNP:170387"
	253708
	/gene="MEFV"
	/allele="T"
	/allele="G"
variation	/db_xref="dbSNP:450021"
	253823
	/allele="G"
	/allele="T"
variation	/db_xref="dbSNP:224234"
	254247
	/allele="A"
	/allele="T"
variation	/db_xref="dbSNP:2550405"
	254326
	/allele="A"
	/allele="G"

```

variation      /db_xref="dbSNP:71999"
                254864
                /allele="A"
                /allele="G"
variation      /db_xref="dbSNP:71998"
                254911
                /allele="C"
                /allele="A"
variation      /db_xref="dbSNP:2680230"
                254922
                /allele="T"
                /allele="C"
variation      /db_xref="dbSNP:2680229"
                255827
                /allele="A"
                /allele="G"
variation      /db_xref="dbSNP:224232"
                256260
                /allele="G"
                /allele="T"
variation      /db_xref="dbSNP:1219163"
                256462
                /allele="A"
                /allele="C"
variation      /db_xref="dbSNP:186493"
                256517
                /allele="T"
                /allele="C"
variation      /db_xref="dbSNP:1231120"
                256814
                /allele="T"
                /allele="C"
variation      /db_xref="dbSNP:1237346"
                259675
                /allele="G"
                /allele="A"
gene           /db_xref="dbSNP:442387"
                260652..272526
                /gene="ZNF200"
                /note="Located on Accession NT_015360"
                /db_xref="LocusID:7752"
                /db_xref="MIM:603231"
mRNA           join(260652..260806,261957..262287,262872..262960,
                263246..263372,271180..272526)
                /gene="ZNF200"
                /product="zinc finger protein 200"
                /note="Derived by automated computational analysis using
                gene prediction method: BLAST. Supporting evidence
                includes similarity to: 1 mRNA"
                /transcript_id="XM_007972.4"
                /db_xref="GI:14777873"
                /db_xref="LocusID:7752"
                /db_xref="MIM:603231"
CDS            join(262041..262287,262872..262960,263246..263372,
                271180..271901)
                /gene="ZNF200"
                /note="Located on Accession NT_015360"
                /codon_start=1
                /protein_id="XP_007972.2"
                /db_xref="GI:14777874"

```


variation /db_xref="LocusID:7752"
 /db_xref="MIM:603231"
263188
 /gene="ZNF200"
 /allele="G"
 /allele="A"
variation /db_xref="dbSNP:2075852"
263902
 /gene="ZNF200"
 /allele="G"
 /allele="C"
variation /db_xref="dbSNP:494394"
264819
 /gene="ZNF200"
 /allele="T"
 /allele="C"
variation /db_xref="dbSNP:401298"
268495
 /gene="ZNF200"
 /allele="T"
 /allele="C"
variation /db_xref="dbSNP:224236"
268666
 /gene="ZNF200"
 /allele="T"
 /allele="C"
variation /db_xref="dbSNP:493542"
268668
 /gene="ZNF200"
 /allele="T"
 /allele="C"
variation /db_xref="dbSNP:493540"
269349
 /gene="ZNF200"
 /allele="T"
 /allele="C"
STS /db_xref="dbSNP:224235"
270177..270268
 /gene="ZNF200"
 /standard_name="SHGC-7172"
STS /db_xref="UniSTS:78933"
272265..272363
 /gene="ZNF200"
 /standard_name="SHGC-60185"
variation /db_xref="UniSTS:50549"
273402
 /allele="G"
 /allele="C"
variation /db_xref="dbSNP:11228"
274571
 /allele="G"
 /allele="A"
variation /db_xref="dbSNP:2238400"
275861
 /allele="G"
 /allele="A"
variation /db_xref="dbSNP:2735545"
277716
 /allele="T"
 /allele="G"

```

variation      /db_xref="dbSNP:2735544"
                277770
                /allele="G"
                /allele="C"
variation      /db_xref="dbSNP:2550402"
                279229
                /allele="T"
                /allele="C"
variation      /db_xref="dbSNP:2179012"
                279241
                /allele="T"
                /allele="C"
gene           /db_xref="dbSNP:2741916"
                complement(279244..280242)
                /gene="OR1F2"
                /note="synonyms: OLFMF2, OR1F2P, OR1F3P; Located on
                Accession NT_015360"
mRNA           /db_xref="LocusID:26184"
                complement(279244..280242)
                /gene="OR1F2"
                /product="olfactory receptor, family 1, subfamily F,
                member 2"
                /note="Derived by automated computational analysis using
                gene prediction method: BLAST. Supporting evidence
                includes similarity to: 2 mRNAs"
                /transcript_id="XM_036497.1"
                /db_xref="GI:14777865"
                /db_xref="LocusID:26184"
CDS            complement(279244..280083)
                /gene="OR1F2"
                /note="Located on Accession NT_015360"
                /codon_start=1
                /protein_id="XP_036497.1"
                /db_xref="GI:14777866"
                /db_xref="LocusID:26184"
variation      279722
                /allele="T"
                /allele="C"
variation      /db_xref="dbSNP:2550401"
                280365
                /allele="G"
                /allele="C"
variation      /db_xref="dbSNP:579134"
                280738
                /allele="T"
                /allele="A"
variation      /db_xref="dbSNP:2113249"
                280816
                /allele="T"
                /allele="G"
variation      /db_xref="dbSNP:2113248"
                283243
                /allele="G"
                /allele="A"
variation      /db_xref="dbSNP:2735542"
                283348
                /allele="T"
                /allele="G"
variation      /db_xref="dbSNP:2735541"
                284042

```

```

/allele="G"
/allele="A"
/db_xref="dbSNP:2741915"
variation 284942
/allele="G"
/allele="A"
/db_xref="dbSNP:2735540"
variation 286120
/allele="G"
/allele="A"
/db_xref="dbSNP:2741914"
variation 286341
/allele="C"
/allele="T"
/db_xref="dbSNP:2550403"
variation 287925
/allele="T"
/allele="C"
/db_xref="dbSNP:548927"
variation 289115
/allele="T"
/allele="C"
/db_xref="dbSNP:2741913"
gene complement(290608..291546)
/allele="OR1F1"
/note="synonyms: OLFMF, OR1F4, OR1F5, OR1F6, OR1F7, OR1F8,
OR1F9, OR16-36, OR16-37, OR16-88, OR16-89, OR16-90;
Located on Accession NT_015360"
/db_xref="LocusID:4992"
/db_xref="MIM:603232"
mRNA complement(290608..291546)
/allele="OR1F1"
/product="olfactory receptor, family 1, subfamily F,
member 1"
/note="Derived by automated computational analysis using
gene prediction method: BLAST. Supporting evidence
includes similarity to: 2 mRNAs"
/transcript_id="NM_012360.1"
/db_xref="GI:6912553"
/db_xref="LocusID:4992"
/db_xref="MIM:603232"
CDS complement(290608..291546)
/allele="OR1F1"
/number=1
/codon_start=1
/product="olfactory receptor, family 1, subfamily F,
member 8"
/protein_id="NP_036492.1"
/db_xref="GI:6912554"
/db_xref="LocusID:4992"
/db_xref="MIM:603232"
variation 290821
/allele="G"
/allele="A"
/db_xref="dbSNP:2075851"
variation 291323
/allele="A"
/allele="G"
/db_xref="dbSNP:1834026"
variation 292660

```

	/allele="C"
	/allele="T"
STS	/db_xref="dbSNP:224176"
	293052..293161
	/standard_name="D16S2617"
	/db_xref="UniSTS:74932"
STS	293053..293184
	/standard_name="D16S2618"
	/db_xref="UniSTS:57086"
variation	293088..293090
	/allele="-"
	/allele="ATT"
	/db_xref="dbSNP:3064192"
variation	293094..293102
	/allele="-"
	/allele="ATTATTATT"
	/db_xref="dbSNP:3064190"
variation	293452
	/allele="T"
	/allele="G"
	/db_xref="dbSNP:885745"
variation	293459
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:885744"
variation	299921
	/allele="T"
	/allele="G"
	/db_xref="dbSNP:434508"
variation	300027
	/allele="C"
	/allele="A"
	/db_xref="dbSNP:374846"
variation	300596
	/allele="G"
	/allele="C"
	/db_xref="dbSNP:2238397"
variation	300599
	/allele="G"
	/allele="C"
	/db_xref="dbSNP:2741911"
variation	301182
	/allele="T"
	/allele="A"
	/db_xref="dbSNP:2238396"
variation	301842
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:403863"
variation	301851
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:402936"
variation	301871
	/allele="T"
	/allele="G"
	/db_xref="dbSNP:437867"
variation	301889
	/allele="C"
	/allele="T"

```

gene      /db_xref="dbSNP:397330"
          complement(302192..340075)
          /gene="LOC124210"
          /note="Located on Accession NT_015360"
          /db_xref="InterimID:124210"
mRNA      complement(join(302192..302421,303824..303870,
          304456..304555,305995..306044,308234..308303,
          312660..312834,320355..320546,321564..321728,
          323780..323981,325040..325220,340033..340075))
          /gene="LOC124210"
          /product="hypothetical gene LOC124210"
          /note="Derived by automated computational analysis using
          gene prediction method: GenomeScan."
          /transcript_id="XM_064031.1"
          /db_xref="GI:17487926"
          /db_xref="InterimID:124210"
CDS       complement(join(302192..302421,303824..303870,
          304456..304555,305995..306044,308234..308303,
          312660..312834,320355..320546,321564..321728,
          323780..323981,325040..325220,340033..340075))
          /gene="LOC124210"
          /note="Located on Accession NT_015360"
          /codon_start=1
          /protein_id="XP_064031.1"
          /db_xref="GI:17487927"
          /db_xref="InterimID:124210"
variation 302831
          /allele="T"
          /allele="G"
          /db_xref="dbSNP:2283473"
variation 302878
          /allele="T"
          /allele="C"
          /db_xref="dbSNP:2283472"
variation 302884
          /allele="G"
          /allele="A"
          /db_xref="dbSNP:2283471"
variation 303101
          /allele="C"
          /allele="A"
          /db_xref="dbSNP:2283470"
variation 303102
          /allele="G"
          /allele="A"
          /db_xref="dbSNP:426866"
variation 303114
          /allele="G"
          /allele="C"
          /db_xref="dbSNP:2283469"
variation 303178
          /allele="G"
          /allele="A"
          /db_xref="dbSNP:427135"
variation 303794
          /allele="G"
          /allele="A"
          /db_xref="dbSNP:2238394"
variation 303818
          /allele="C"

```

variation /allele="A"
/db_xref="dbSNP:2238393"
303839
/allele="G"
/allele="C"
variation /db_xref="dbSNP:2238392"
303888
/allele="G"
/allele="C"
variation /db_xref="dbSNP:450623"
304778
/allele="C"
/allele="T"
variation /db_xref="dbSNP:366494"
304832
/allele="C"
/allele="G"
variation /db_xref="dbSNP:382077"
305247
/allele="A"
/allele="T"
variation /db_xref="dbSNP:424599"
305496
/allele="T"
/allele="C"
variation /db_xref="dbSNP:377048"
305539
/allele="A"
/allele="G"
variation /db_xref="dbSNP:412836"
305978
/allele="G"
/allele="A"
variation /db_xref="dbSNP:2238391"
306275
/allele="A"
/allele="G"
variation /db_xref="dbSNP:393461"
307959
/allele="A"
/allele="G"
variation /db_xref="dbSNP:415846"
308006
/allele="A"
/allele="G"
variation /db_xref="dbSNP:417848"
308016
/allele="T"
/allele="A"
variation /db_xref="dbSNP:2238390"
308212
/allele="A"
/allele="G"
variation /db_xref="dbSNP:424165"
308450
/allele="G"
/allele="A"
variation /db_xref="dbSNP:2238389"
308522
/allele="C"

variation /allele="T"
/db_xref="dbSNP:370323"
308926

variation /allele="G"
/allele="A"
/db_xref="dbSNP:2238388"
308987

variation /allele="G"
/allele="A"
/db_xref="dbSNP:508099"
309542

variation /allele="G"
/allele="C"
/db_xref="dbSNP:909403"
310248

variation /allele="A"
/allele="G"
/db_xref="dbSNP:372163"
311348

variation /allele="T"
/allele="A"
/db_xref="dbSNP:224184"
311389

variation /allele="C"
/allele="T"
/db_xref="dbSNP:2013522"
311576

variation /allele="G"
/allele="A"
/db_xref="dbSNP:224183"
311683

variation /allele="T"
/allele="A"
/db_xref="dbSNP:2013328"
312056

variation /allele="T"
/allele="G"
/db_xref="dbSNP:172787"
312378

variation /allele="G"
/allele="C"
/db_xref="dbSNP:2238387"
314793..314794

variation /allele="-"
/allele="AA"
/db_xref="dbSNP:3064159"
315209

variation /allele="G"
/allele="C"
/db_xref="dbSNP:1559386"
315321

variation /allele="G"
/allele="C"
/db_xref="dbSNP:1002965"
316849

variation /allele="G"
/allele="A"
/db_xref="dbSNP:170380"
317280

variation /allele="C"

	/allele="A"
	/db_xref="dbSNP:2741910"
variation	318538
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:224202"
variation	318760
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:178617"
variation	318865
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:224201"
variation	318924
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:224200"
variation	319292
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:909194"
variation	319924
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:224199"
variation	322768
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:224198"
variation	323432
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:224197"
variation	323484
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:224196"
variation	323841
	/allele="A"
	/allele="C"
	/db_xref="dbSNP:2544572"
variation	326193
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:2741907"
variation	327878
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:2741906"
variation	328179
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:2741904"
variation	329242
	/allele="G"
	/allele="C"
	/db_xref="dbSNP:2741902"
variation	329682
	/allele="G"

variation /allele="T"
/db_xref="dbSNP:224195"
330075
/allele="A"
/allele="G"
variation /db_xref="dbSNP:224194"
330236
/allele="T"
/allele="C"
variation /db_xref="dbSNP:2741901"
330330
/allele="C"
/allele="G"
variation /db_xref="dbSNP:190115"
330437
/allele="C"
/allele="T"
variation /db_xref="dbSNP:224193"
330530
/allele="A"
/allele="C"
variation /db_xref="dbSNP:2717707"
330583
/allele="A"
/allele="G"
variation /db_xref="dbSNP:1816115"
330688
/allele="G"
/allele="A"
variation /db_xref="dbSNP:2741900"
330828
/allele="C"
/allele="T"
variation /db_xref="dbSNP:1816116"
331350
/allele="C"
/allele="A"
variation /db_xref="dbSNP:2252009"
331440
/allele="A"
/allele="C"
variation /db_xref="dbSNP:224192"
332429
/allele="C"
/allele="T"
variation /db_xref="dbSNP:2550393"
332454
/allele="C"
/allele="T"
variation /db_xref="dbSNP:2550394"
332878
/allele="G"
/allele="C"
variation /db_xref="dbSNP:2735527"
333231
/allele="A"
/allele="C"
variation /db_xref="dbSNP:2717708"
333242
/allele="A"

	/allele="C"
	/db_xref="dbSNP:192005"
variation	333250
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:2741899"
variation	333294
	/allele="A"
	/allele="C"
	/db_xref="dbSNP:178616"
variation	333403
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:172789"
variation	335667
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:438927"
variation	335769
	/allele="T"
	/allele="G"
	/db_xref="dbSNP:2741898"
variation	335889
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:2717665"
variation	335948
	/allele="G"
	/allele="C"
	/db_xref="dbSNP:1977011"
variation	336777
	/allele="G"
	/allele="C"
	/db_xref="dbSNP:2735526"
variation	336858
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:2223169"
variation	336861
	/allele="C"
	/allele="T"
	/db_xref="dbSNP:2717666"
variation	336876
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:2735525"
variation	336933
	/allele="T"
	/allele="A"
	/db_xref="dbSNP:2205555"
variation	337914
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:2981598"
variation	337946
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:2981597"
variation	337952
	/allele="T"

variation /allele="G"
/db_xref="dbSNP:2981596"
337954

variation /allele="C"
/allele="A"
/db_xref="dbSNP:2142472"
337977

variation /allele="G"
/allele="A"
/db_xref="dbSNP:2142471"
338355

variation /allele="C"
/allele="T"
/db_xref="dbSNP:2717667"
339369

variation /allele="C"
/allele="T"
/db_xref="dbSNP:224190"
340407

variation /allele="C"
/allele="T"
/db_xref="dbSNP:2194335"
340454

variation /allele="A"
/allele="T"
/db_xref="dbSNP:2194336"
340467

variation /allele="A"
/allele="C"
/db_xref="dbSNP:2194337"
340974

variation /allele="A"
/allele="G"
/db_xref="dbSNP:2550406"
341075

variation /allele="C"
/allele="T"
/db_xref="dbSNP:170381"
341708

variation /allele="T"
/allele="C"
/db_xref="dbSNP:415809"
341709

variation /allele="G"
/allele="C"
/db_xref="dbSNP:434205"
341995

variation /allele="C"
/allele="G"
/db_xref="dbSNP:224189"
342094

variation /allele="G"
/allele="C"
/db_xref="dbSNP:2741897"
342467

variation /allele="A"
/allele="G"
/db_xref="dbSNP:224188"
342509

variation /allele="C"

	/allele="T"
	/db_xref="dbSNP:224187"
variation	342541
	/allele="T"
	/allele="A"
	/db_xref="dbSNP:2735523"
variation	342738
	/allele="A"
	/allele="G"
	/db_xref="dbSNP:224186"
variation	342767
	/allele="A"
	/allele="C"
	/db_xref="dbSNP:224185"
variation	343524
	/allele="T"
	/allele="A"
	/db_xref="dbSNP:2741894"
variation	343873
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:2735522"
variation	343898
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:2735521"
variation	344267
	/allele="G"
	/allele="T"
	/db_xref="dbSNP:172788"
variation	344373
	/allele="T"
	/allele="G"
	/db_xref="dbSNP:2741893"
variation	344451
	/allele="C"
	/allele="A"
	/db_xref="dbSNP:2735518"
variation	344467
	/allele="C"
	/allele="A"
	/db_xref="dbSNP:2735517"
variation	344540
	/allele="G"
	/allele="C"
	/db_xref="dbSNP:2741892"
variation	344889
	/allele="G"
	/allele="C"
	/db_xref="dbSNP:2741890"
variation	344890
	/allele="G"
	/allele="C"
	/db_xref="dbSNP:2735516"
variation	344911
	/allele="G"
	/allele="C"
	/db_xref="dbSNP:2238386"
variation	345132
	/allele="T"

	/allele="C"
	/db_xref="dbSNP:2735515"
variation	345512
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:224245"
STS	345752..345855
	/standard_name="RH120131"
	/db_xref="UniSTS:132336"
variation	346079
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:2735514"
variation	346263
	/allele="T"
	/allele="C"
	/db_xref="dbSNP:224244"
variation	346569
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:2735513"
variation	346639
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:2735512"
variation	346674
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:2238385"
variation	346796
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:2735510"
variation	346854
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:551848"
variation	346859
	/allele="T"
	/allele="G"
	/db_xref="dbSNP:551845"
variation	346880
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:2735509"
variation	346886
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:2735508"
variation	348169
	/allele="G"
	/allele="A"
	/db_xref="dbSNP:2735507"
variation	348290
	/allele="T"
	/allele="G"
	/db_xref="dbSNP:2735506"
variation	349457
	/allele="C"
	/allele="A"

variation /db_xref="dbSNP:2859692"
349523
/allele="T"
/allele="C"

variation /db_xref="dbSNP:2735504"
350418
/allele="C"
/allele="A"

variation /db_xref="dbSNP:2735503"
350524
/allele="C"
/allele="A"

variation /db_xref="dbSNP:2735502"
350730
/allele="T"
/allele="C"

variation /db_xref="dbSNP:2238384"
350742
/allele="T"
/allele="G"

variation /db_xref="dbSNP:2735501"
350815
/allele="C"
/allele="A"

variation /db_xref="dbSNP:2238383"
350821
/allele="T"
/allele="A"

variation /db_xref="dbSNP:2238382"
350962
/allele="T"
/allele="C"

variation /db_xref="dbSNP:2238381"
351111
/allele="G"
/allele="C"

variation /db_xref="dbSNP:2735555"
351135
/allele="G"
/allele="C"

variation /db_xref="dbSNP:224249"
351176
/allele="T"
/allele="C"

variation /db_xref="dbSNP:2550392"
351393
/allele="G"
/allele="A"

variation /db_xref="dbSNP:2550391"
351452
/allele="G"
/allele="A"

variation /db_xref="dbSNP:2550390"
352023
/allele="G"
/allele="A"

variation /db_xref="dbSNP:2717711"
352082
/allele="G"
/allele="C"

variation /db_xref="dbSNP:2717710"
352093
/allele="G"
/allele="A"
variation /db_xref="dbSNP:2735550"
352159
/allele="C"
/allele="A"
variation /db_xref="dbSNP:2735549"
352217
/allele="T"
/allele="A"
variation /db_xref="dbSNP:2238380"
352331
/allele="T"
/allele="C"
variation /db_xref="dbSNP:2238379"
352575
/allele="T"
/allele="C"
variation /db_xref="dbSNP:2238378"
352874
/allele="T"
/allele="C"
gene /db_xref="dbSNP:2717709"
complement(352988..360867)
/gene="ZNF213"
/note="synonym: CR53; Located on Accession NT_015360"
/db_xref="LocusID:7760"
mRNA complement(join(352988..355100,356691..356814,
356971..357044,357248..357371,358110..358623,
360402..360476,360687..360867))
/gene="ZNF213"
/product="zinc finger protein 213"
/note="Derived by automated computational analysis using
gene prediction method: BLAST. Supporting evidence
includes similarity to: 5 mRNAs"
/transcript_id="XM_036493.1"
/db_xref="GI:14777853"
/db_xref="LocusID:7760"
variation 353051
/allele="G"
/allele="C"
variation /db_xref="dbSNP:1053998"
353119
/allele="G"
/allele="A"
variation /db_xref="dbSNP:1053997"
353141
/allele="G"
/allele="A"
variation /db_xref="dbSNP:1053996"
353331
/allele="T"
/allele="C"
variation /db_xref="dbSNP:1063941"
353337
/allele="T"
/allele="C"
/db_xref="dbSNP:1063940"

```

variation      353507
                /allele="T"
                /allele="G"
                /db_xref="dbSNP:385343"
variation      353565
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:418847"
variation      354284
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:224248"
variation      354309
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:224247"
variation      354434
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:2735537"
CDS            complement(join(354442..355100,356691..356814,
                356971..357044,357248..357371,358110..358508))
                /gene="ZNF213"
                /note="Located on Accession NT_015360"
                /codon_start=1
                /protein_id="XP_036493.1"
                /db_xref="GI:14777854"
                /db_xref="LocusID:7760"
variation      355455
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:2550389"
variation      356345
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:172792"
variation      356411
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:224246"
variation      356488
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:2735536"
variation      356569
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:2735535"
variation      356679
                /allele="G"
                /allele="C"
                /db_xref="dbSNP:2735534"
variation      356846
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:2735533"
variation      356966
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:2735532"

```


variation	358023 /allele="C" /allele="T" /db_xref="dbSNP:2717686"
variation	358105 /allele="C" /allele="T" /db_xref="dbSNP:2717687"
variation	360053 /allele="G" /allele="A" /db_xref="dbSNP:560947"
variation	360143 /allele="G" /allele="A" /db_xref="dbSNP:2735539"
variation	360148 /allele="G" /allele="T" /db_xref="dbSNP:2717698"
variation	360177 /allele="C" /allele="A" /db_xref="dbSNP:2735538"
variation	360309 /allele="C" /allele="T" /db_xref="dbSNP:2717699"
variation	360472 /allele="T" /allele="C" /db_xref="dbSNP:2741934"
variation	360535 /allele="C" /allele="A" /db_xref="dbSNP:2205556"
variation	362229 /allele="G" /allele="T" /db_xref="dbSNP:192006"
variation	363830 /allele="A" /allele="G" /db_xref="dbSNP:1053871"
variation	364201 /allele="C" /allele="T" /db_xref="dbSNP:224238"
variation	364256 /allele="C" /allele="T" /db_xref="dbSNP:224237"
variation	365426 /allele="G" /allele="C" /db_xref="dbSNP:426827"
variation	367196 /allele="T" /allele="G" /db_xref="dbSNP:1883026"

variation	369952 /allele="C" /allele="T" /db_xref="dbSNP:1064269"
variation	370053 /allele="C" /allele="T" /db_xref="dbSNP:1057160"
variation	370865 /allele="G" /allele="C" /db_xref="dbSNP:926187"
variation	371250 /allele="T" /allele="C" /db_xref="dbSNP:443540"
variation	371476 /allele="C" /allele="A" /db_xref="dbSNP:382073"
variation	371849 /allele="T" /allele="C" /db_xref="dbSNP:447195"
variation	371855 /allele="T" /allele="C" /db_xref="dbSNP:378056"
variation	371857 /allele="T" /allele="C" /db_xref="dbSNP:423579"
variation	372221 /allele="G" /allele="C" /db_xref="dbSNP:409646"
variation	372228 /allele="T" /allele="C" /db_xref="dbSNP:443932"
variation	373178 /allele="G" /allele="A" /db_xref="dbSNP:2981600"
variation	373907 /allele="C" /allele="G" /db_xref="dbSNP:741943"
variation	374364 /allele="T" /allele="C" /db_xref="dbSNP:125774"
variation	374395 /allele="G" /allele="A" /db_xref="dbSNP:2006230"
variation	374490 /allele="G" /allele="C" /db_xref="dbSNP:2006229"

```

variation      374685
                /allele="C"
                /allele="A"
                /db_xref="dbSNP:125773"
gene           complement(375285..383198)
                /gene="ZNF205"
                /note="synonym: ZNF210; Located on Accession NT_015360"
                /db_xref="LocusID:7755"
                /db_xref="MIM:603436"
mRNA           complement(join(375285..376544,376785..376895,
                379257..379377,379884..379975,380235..380448,
                382316..382454,383121..383198))
                /gene="ZNF205"
                /product="zinc finger protein 205"
                /note="unclassified transcription discrepancy; Derived by
                automated computational analysis using gene prediction
                method: BLAST. Supporting evidence includes similarity to:
                1 mRNA"
                /transcript_id="NM_003456.1"
                /db_xref="GI:4508014"
                /db_xref="LocusID:7755"
                /db_xref="MIM:603436"
STS           375288..375480
                /standard_name="STS-W93354"
                /db_xref="UniSTS:57067"
CDS           complement(join(375475..376544,376785..376895,
                379257..379377,379884..379975,380235..380355))
                /gene="ZNF205"
                /note="zinc finger type C2H2; contains KRAB domain; zinc
                finger protein 210"
                /codon_start=1
                /product="zinc finger protein 205"
                /protein_id="NP_003447.1"
                /db_xref="GI:4508015"
                /db_xref="LocusID:7755"
                /db_xref="MIM:603436"
variation      375613
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:12032"
variation      376965
                /allele="C"
                /allele="A"
                /db_xref="dbSNP:224181"
variation      377076
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:224180"
variation      377734
                /allele="G"
                /allele="C"
                /db_xref="dbSNP:224179"
variation      379218
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:224178"
variation      379661
                /allele="C"
                /allele="A"
                /db_xref="dbSNP:2294150"

```

```

variation      380121
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:2280951"
gene           380203..385342
                /gene="MGC3771"
                /note="synonym: MGC1912; Located on Accession NT_015360"
                /db_xref="LocusID:81854"
mRNA           join(380203..380835,380916..381008,384849..385342)
                /gene="MGC3771"
                /product="hypothetical protein MGC3771"
                /note="Derived by automated computational analysis using
                gene prediction method: BLAST. Supporting evidence
                includes similarity to: 2 mRNAs"
                /transcript_id="XM_036491.1"
                /db_xref="GI:14777842"
                /db_xref="LocusID:81854"
variation      380379
                /gene="MGC3771"
                /note="WARNING: map location ambiguous"
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:909410"
variation      380753
                /gene="MGC3771"
                /note="WARNING: map location ambiguous"
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:224177"
variation      381105
                /gene="MGC3771"
                /note="WARNING: map location ambiguous"
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:2002341"
variation      381524
                /gene="MGC3771"
                /note="WARNING: map location ambiguous"
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:125772"
STS           382403..382729
                /gene="MGC3771"
                /standard_name="RH119820"
                /note="WARNING: map location ambiguous"
                /db_xref="UniSTS:133510"
variation      382666
                /gene="MGC3771"
                /note="WARNING: map location ambiguous"
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:2280950"
gene           383314..385291
                /gene="LOC146438"
                /note="Located on Accession NT_015360"
                /db_xref="InterimID:146438"
mRNA           join(383314..383520,384849..385291)
                /gene="LOC146438"
                /product="similar to PRO2550"
                /note="Derived by automated computational analysis using

```

```

gene prediction method: BLAST."
/transcript_id="XM_085464.1"
/db_xref="GI:18585770"
/db_xref="InterimID:146438"
CDS join(383374..383520,384849..385088)
    /gene="LOC146438"
    /note="Located on Accession NT_015360"
    /codon_start=1
    /protein_id="XP_085464.1"
    /db_xref="GI:18585771"
    /db_xref="InterimID:146438"
variation 384113
    /gene="LOC146438"
    /note="WARNING: map location ambiguous"
    /allele="G"
    /allele="C"
    /db_xref="dbSNP:2741933"
CDS 385014..385088
    /gene="LOC146438"
    /note="Located on Accession NT_015360"
    /codon_start=1
    /protein_id="XP_036491.1"
    /db_xref="GI:14777843"
    /db_xref="InterimID:146438"
gene 386361..394632
    /gene="LOC124212"
    /note="Located on Accession NT_015360"
    /db_xref="InterimID:124212"
mRNA join(386361..386409,389194..389324,394330..394388,
    394524..394632)
    /gene="LOC124212"
    /product="hypothetical gene LOC124212"
    /note="Derived by automated computational analysis using
    gene prediction method: GenomeScan."
    /transcript_id="XM_064032.1"
    /db_xref="GI:17487928"
    /db_xref="InterimID:124212"
CDS join(386361..386409,389194..389324,394330..394388,
    394524..394632)
    /gene="LOC124212"
    /note="Located on Accession NT_015360"
    /codon_start=1
    /protein_id="XP_064032.1"
    /db_xref="GI:17487929"
    /db_xref="InterimID:124212"
variation 389213
    /gene="LOC124212"
    /allele="T"
    /allele="C"
    /db_xref="dbSNP:2294149"
variation 392402
    /gene="LOC124212"
    /allele="T"
    /allele="C"
    /db_xref="dbSNP:2741932"
variation 392608
    /gene="LOC124212"
    /allele="T"
    /allele="G"
    /db_xref="dbSNP:2741931"

```

```

variation      393575
                /gene="LOC124212"
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:731045"
variation      394472
                /gene="LOC124212"
                /allele="A"
                /allele="G"
                /db_xref="dbSNP:2717694"
variation      394912
                /allele="G"
                /allele="T"
                /db_xref="dbSNP:2717695"
variation      396036
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:909407"
variation      396292
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:909406"
variation      396819
                /allele="C"
                /allele="A"
                /db_xref="dbSNP:909405"
variation      397088
                /allele="G"
                /allele="C"
                /db_xref="dbSNP:2741930"
variation      398136
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:2717685"
variation      399526
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:2037984"
variation      399783
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:2037983"
variation      400027
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:2056891"
variation      401344
                /allele="C"
                /allele="G"
                /db_xref="dbSNP:2017820"
gene           402953..406919
                /gene="FLJ14549"
                /note="Located on Accession NT_015360"
                /db_xref="LocusID:84891"
mRNA           join(402953..403271,403497..403764,403985..404049,
                404216..404273,405167..406919)
                /gene="FLJ14549"
                /product="hypothetical protein FLJ14549"
                /note="unclassified transcription discrepancy; Derived by
                automated computational analysis using gene prediction

```

```

method: BLAST. Supporting evidence includes similarity to:
2 mRNAs"
/transcript_id="NM_032805.1"
/db_xref="GI:14249487"
/db_xref="LocusID:84891"
CDS      join(403041..403271,403497..403764,403985..404049,
404216..404273,405167..406722)
/gene="FLJ14549"
/codon_start=1
/evidence=not_experimental
/product="hypothetical protein FLJ14549"
/protein_id="NP_116194.1"
/db_xref="GI:14249488"
/db_xref="LocusID:84891"
STS      406715..406851
/gene="FLJ14549"
/standard_name="RH91869"
/db_xref="UniSTS:89322"
variation 409291
/allele="G"
/allele="C"
/db_xref="dbSNP:909404"
variation 410679
/allele="T"
/allele="C"
/db_xref="dbSNP:2092016"
variation 411060
/allele="T"
/allele="C"
/db_xref="dbSNP:2092015"
variation 412296
/allele="T"
/allele="C"
/db_xref="dbSNP:2360173"
STS      413634..413814
/standard_name="STS-M59807"
/note="WARNING: map location ambiguous"
/db_xref="UniSTS:12359"
variation 413787
/note="WARNING: map location ambiguous"
/allele="T"
/allele="G"
/db_xref="dbSNP:2472684"
gene      complement(413853..420635)
/gene="LOC124213"
/note="Located on Accession NT_015360"
/db_xref="InterimID:124213"
mRNA      complement(join(413853..414179,420474..420635))
/gene="LOC124213"
/product="similar to natural killer cell transcript 4"
/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_064033.1"
/db_xref="GI:17487930"
/db_xref="InterimID:124213"
CDS      complement(join(413853..414179,420474..420635))
/gene="LOC124213"
/note="Located on Accession NT_015360"
/codon_start=1
/protein_id="XP_064033.1"

```

variation /db_xref="GI:17487931"
/db_xref="InterimID:124213"
413867
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:2981599"
variation 413876
/note="WARNING: map location ambiguous"
/allele="T"
/allele="G"
/db_xref="dbSNP:2741929"
variation 413918
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:2741928"
variation 414247
/allele="C"
/allele="A"
/db_xref="dbSNP:2741927"
variation 414354
/allele="G"
/allele="T"
/db_xref="dbSNP:1985852"
variation 417873
/allele="G"
/allele="A"
/db_xref="dbSNP:1985560"
variation 418365
/allele="G"
/allele="A"
/db_xref="dbSNP:2005948"
variation 418959
/allele="G"
/allele="A"
/db_xref="dbSNP:2360171"
variation 419114
/allele="T"
/allele="C"
/db_xref="dbSNP:760413"
variation 419122
/allele="T"
/allele="G"
/db_xref="dbSNP:760412"
variation 420098
/allele="T"
/allele="C"
/db_xref="dbSNP:2360170"
variation 420260
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:2075850"
variation 420890
/allele="T"
/allele="C"
/db_xref="dbSNP:1534865"
variation 421102
/allele="T"

variation /allele="C"
/db_xref="dbSNP:1969616"
422251
/allele="T"
/allele="A"
variation /db_xref="dbSNP:2015620"
422399
/allele="T"
/allele="C"
variation /db_xref="dbSNP:2717681"
422473
/allele="C"
/allele="G"
variation /db_xref="dbSNP:2717688"
422508
/allele="G"
/allele="T"
variation /db_xref="dbSNP:2717689"
422545
/allele="A"
/allele="T"
variation /db_xref="dbSNP:2717690"
422739
/note="WARNING: map location ambiguous"
/allele="G"
/allele="C"
variation /db_xref="dbSNP:2741903"
422812
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
variation /db_xref="dbSNP:2717680"
422989
/note="WARNING: map location ambiguous"
/allele="T"
/allele="G"
variation /db_xref="dbSNP:2259214"
423167
/note="WARNING: map location ambiguous"
/allele="G"
/allele="C"
variation /db_xref="dbSNP:2257551"
423407
/note="WARNING: map location ambiguous"
/allele="G"
/allele="C"
variation /db_xref="dbSNP:2223170"
/db_xref="dbSNP:2717679"
423522
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
variation /db_xref="dbSNP:2717671"
/db_xref="dbSNP:2717678"
423715
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
variation /db_xref="dbSNP:2717670"
423748

```

variation    /note="WARNING: map location ambiguous"
              /allele="T"
              /allele="C"
              /db_xref="dbSNP:2717669"
              423749
              /note="WARNING: map location ambiguous"
              /allele="G"
              /allele="C"
              /db_xref="dbSNP:2741925"
variation    423797
              /allele="T"
              /allele="C"
              /db_xref="dbSNP:2015174"
variation    423810
              /allele="G"
              /allele="A"
              /db_xref="dbSNP:2717677"
variation    425966
              /allele="T"
              /allele="C"
              /db_xref="dbSNP:1810409"
gene          complement(426262..430150)
              /gene="NK4"
              /note="Located on Accession NT_015360"
              /db_xref="LocusID:9235"
              /db_xref="MIM:606001"
mRNA          complement(join(426262..426822,427573..427632,
              427802..427828,428199..428435,429988..430030,
              430127..430150))
              /gene="NK4"
              /product="natural killer cell transcript 4"
              /note="unclassified transcription discrepancy; Derived by
              automated computational analysis using gene prediction
              method: BLAST. Supporting evidence includes similarity to:
              1 mRNA"
              /transcript_id="NM_004221.1"
              /db_xref="GI:4758811"
              /db_xref="LocusID:9235"
              /db_xref="MIM:606001"
STS          426276..426456
              /standard_name="STS-M59807"
              /note="WARNING: map location ambiguous"
              /db_xref="UniSTS:12359"
variation    426429
              /note="WARNING: map location ambiguous"
              /allele="T"
              /allele="G"
              /db_xref="dbSNP:2472684"
CDS          complement(join(426457..426822,427573..427632,
              427802..427828,428199..428435,429988..430002))
              /gene="NK4"
              /note="unclassified translation discrepancy"
              /codon_start=1
              /product="natural killer cell transcript 4"
              /protein_id="NP_004212.2"
              /db_xref="GI:11072104"
              /db_xref="LocusID:9235"
              /db_xref="MIM:606001"
variation    426509
              /note="WARNING: map location ambiguous"

```

```

/allele="T"
/allele="C"
/db_xref="dbSNP:2981599"
variation 426519
/allele="T"
/allele="G"
/db_xref="dbSNP:2741929"
variation 426561
/allele="G"
/allele="A"
/db_xref="dbSNP:2741928"
variation 427277
/allele="T"
/allele="G"
/db_xref="dbSNP:2717675"
variation 427876
/allele="T"
/allele="C"
/db_xref="dbSNP:2239303"
variation 427936
/allele="T"
/allele="C"
/db_xref="dbSNP:2239302"
STS 428435..428634
/standard_name="D16S3082"
/db_xref="UniSTS:33443"
variation 428459
/allele="T"
/allele="A"
/db_xref="dbSNP:1555001"
variation 428501..428502
/allele="-"
/allele="ACACAC"
/db_xref="dbSNP:3063339"
variation 428694
/allele="T"
/allele="A"
/db_xref="dbSNP:1467384"
variation 428697
/allele="G"
/allele="A"
/db_xref="dbSNP:2717673"
variation 428734
/allele="T"
/allele="A"
/db_xref="dbSNP:1555000"
variation 428774
/allele="T"
/allele="A"
/db_xref="dbSNP:2179015"
variation 428854
/allele="T"
/allele="A"
/db_xref="dbSNP:2179014"
variation 428857
/allele="G"
/allele="A"
/db_xref="dbSNP:2179013"

```

```

variation      429008
                /allele="T"
                /allele="G"
                /db_xref="dbSNP:2717672"
variation      429559
                /allele="C"
                /allele="A"
                /db_xref="dbSNP:2239301"
variation      430187
                /allele="T"
                /allele="G"
                /db_xref="dbSNP:1554999"
variation      431738
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:1534864"
STS            435116..435277
                /standard_name="SHGC-61127"
                /db_xref="UniSTS:16544"
variation      435293
                /allele="T"
                /allele="A"
                /db_xref="dbSNP:1043298"
variation      437539
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:2142475"
variation      437650
                /allele="T"
                /allele="G"
                /db_xref="dbSNP:2142474"
variation      437651
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:2142473"
gene           complement(438492..448263)
                /gene="MMPL1"
                /note="synonym: MMP20; Located on Accession NT_015360"
                /db_xref="LocusID:4328"
mRNA           complement(join(438492..439979,445263..445555,
                445665..445800,448247..448263))
                /gene="MMPL1"
                /product="matrix metalloproteinase-like 1"
                /note="Derived by automated computational analysis using
                gene prediction method: BLAST. Supporting evidence
                includes similarity to: 1 mRNA"
                /transcript_id="NM_004142.1"
                /db_xref="GI:4758727"
                /db_xref="LocusID:4328"
variation      438543
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:2741912"
variation      438820
                /allele="T"
                /allele="A"
                /db_xref="dbSNP:1064948"
STS            438862..439008
                /standard_name="SGC32543"
                /db_xref="UniSTS:99836"

```

```

variation      438921
                /allele="C"
                /allele="A"
                /db_xref="dbSNP:760410"
STS           438923..439045
                /standard_name="RH68424"
                /db_xref="UniSTS:41991"
variation      439146
                /allele="C"
                /allele="G"
                /db_xref="dbSNP:741942"
CDS           complement(join(439861..439979,445263..445555,
                445665..445800,448247..448250))
                /gene="MMPL1"
                /note="matrix metalloproteinase 20"
                /codon_start=1
                /product="matrix metalloproteinase-like 1"
                /protein_id="NP_004133.1"
                /db_xref="GI:4758728"
                /db_xref="LocusID:4328"
variation      440085
                /note="WARNING: map location ambiguous"
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:2075850"
variation      440965
                /allele="G"
                /allele="C"
                /db_xref="dbSNP:2013921"
variation      441045
                /allele="G"
                /allele="C"
                /db_xref="dbSNP:2013916"
variation      441060
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:2013915"
variation      442217
                /allele="G"
                /allele="C"
                /db_xref="dbSNP:2884918"
variation      442333
                /allele="C"
                /allele="A"
                /db_xref="dbSNP:2741905"
variation      442372
                /note="WARNING: map location ambiguous"
                /allele="G"
                /allele="C"
                /db_xref="dbSNP:2741903"
variation      442445
                /note="WARNING: map location ambiguous"
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:2717680"
variation      442622
                /note="WARNING: map location ambiguous"
                /allele="T"
                /allele="G"
                /db_xref="dbSNP:2259214"

```

variation 442800
/note="WARNING: map location ambiguous"
/allele="G"
/allele="C"
/db_xref="dbSNP:2257551"

variation 442801
/allele="G"
/allele="A"
/db_xref="dbSNP:1969615"

variation 443040
/note="WARNING: map location ambiguous"
/allele="G"
/allele="C"
/db_xref="dbSNP:2223170"
/db_xref="dbSNP:2717679"

variation 443155
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:2717671"
/db_xref="dbSNP:2717678"

variation 443348
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:2717670"

variation 443381
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:2717669"

variation 443382
/note="WARNING: map location ambiguous"
/allele="G"
/allele="C"
/db_xref="dbSNP:2741925"

variation 443603
/allele="C"
/allele="T"
/db_xref="dbSNP:1064875"

variation 443636
/allele="G"
/allele="T"
/db_xref="dbSNP:1061019"

variation 443785
/allele="G"
/allele="C"
/db_xref="dbSNP:2741896"

variation 443848
/allele="G"
/allele="A"
/db_xref="dbSNP:2741895"

variation 443992
/allele="T"
/allele="C"
/db_xref="dbSNP:2741891"

variation 445657
/allele="G"
/allele="C"
/db_xref="dbSNP:2717668"

```

variation      446368
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:2247226"
variation      447170
                /allele="C"
                /allele="A"
                /db_xref="dbSNP:2360168"
variation      448339
                /allele="G"
                /allele="C"
                /db_xref="dbSNP:2142477"
variation      448400
                /allele="T"
                /allele="G"
                /db_xref="dbSNP:909409"
variation      448500
                /allele="A"
                /allele="G"
                /db_xref="dbSNP:879734"
variation      448721
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:909408"
variation      448932
                /allele="C"
                /allele="A"
                /db_xref="dbSNP:2250306"
variation      449636
                /allele="C"
                /allele="A"
                /db_xref="dbSNP:2360167"
variation      451534
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:1004792"
STS            451744..451944
                /standard_name="D16S468"
                /db_xref="UniSTS:148327"
STS            451762..451924
                /standard_name="D16S3070"
                /db_xref="UniSTS:24815"
variation      452966
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:2360166"
variation      453285
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:2360165"
variation      453403
                /allele="T"
                /allele="A"
                /db_xref="dbSNP:2360164"
variation      453432
                /allele="A"
                /allele="G"
                /db_xref="dbSNP:2717691"
variation      455279
                /note="WARNING: map location ambiguous"

```

```

/allele="T"
/allele="C"
/db_xref="dbSNP:909410"
variation 455653
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:224177"
variation 456005
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:2002341"
variation 456424
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:125772"
STS 457303..457629
/standard_name="RH119820"
/note="WARNING: map location ambiguous"
/db_xref="UniSTS:133510"
variation 457566
/note="WARNING: map location ambiguous"
/allele="T"
/allele="C"
/db_xref="dbSNP:2280950"
variation 459013
/note="WARNING: map location ambiguous"
/allele="G"
/allele="C"
/db_xref="dbSNP:2741933"
variation 460492
/note="WARNING: map location ambiguous"
/allele="G"
/allele="A"
/db_xref="dbSNP:1859376"
variation 461503
/note="WARNING: map location ambiguous"
/allele="T"
/allele="A"
/db_xref="dbSNP:2526261"
variation 461669
/note="WARNING: map location ambiguous"
/allele="T"
/allele="G"
/db_xref="dbSNP:1972513"
variation 463114
/allele="G"
/allele="A"
/db_xref="dbSNP:2878533"
variation 463888
/note="WARNING: map location ambiguous"
/allele="A"
/allele="C"
/db_xref="dbSNP:1972513"
variation 464377
/note="WARNING: map location ambiguous"
/allele="A"
/allele="T"

```


variation /db_xref="dbSNP:2526261"
465388
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
/db_xref="dbSNP:1859376"
gene 466644..472860
/gene="LOC146439"
/note="Located on Accession NT_015360"
/db_xref="InterimID:146439"
mRNA join(466644..466676,468044..468355,472413..472628,
472751..472860)
/gene="LOC146439"
/product="LOC146439"
/note="Derived by automated computational analysis using
gene prediction method: BLAST."
/transcript_id="XM_085463.1"
/db_xref="GI:18585772"
/db_xref="InterimID:146439"
variation 468486
/gene="LOC146439"
/allele="C"
/allele="G"
/db_xref="dbSNP:732261"
variation 468827
/gene="LOC146439"
/allele="A"
/allele="G"
/db_xref="dbSNP:2428675"
variation 469454
/gene="LOC146439"
/allele="C"
/allele="T"
/db_xref="dbSNP:2526275"
variation 469508
/gene="LOC146439"
/allele="A"
/allele="C"
/db_xref="dbSNP:2526276"
variation 469589
/gene="LOC146439"
/allele="A"
/allele="T"
/db_xref="dbSNP:2526277"
variation 469955
/gene="LOC146439"
/allele="A"
/allele="G"
/db_xref="dbSNP:2526278"
variation 471086
/gene="LOC146439"
/allele="A"
/allele="G"
/db_xref="dbSNP:2526279"
variation 471225
/gene="LOC146439"
/allele="C"
/allele="T"
/db_xref="dbSNP:2717712"
variation 471237

```

/ gene="LOC146439"
/ allele="A"
/ allele="G"
/ db_xref="dbSNP:2717713"
variation 471407
/ gene="LOC146439"
/ allele="C"
/ allele="T"
/ db_xref="dbSNP:2526280"
CDS join(472432..472628,472751..472838)
/ gene="LOC146439"
/ note="Located on Accession NT_015360"
/ codon_start=1
/ protein_id="XP_085463.1"
/ db_xref="GI:18585773"
/ db_xref="InterimID:146439"
variation 473879
/ allele="A"
/ allele="G"
/ db_xref="dbSNP:2244494"
variation 474552
/ allele="C"
/ allele="G"
/ db_xref="dbSNP:2011561"
variation 475017
/ allele="A"
/ allele="C"
/ db_xref="dbSNP:2079244"
variation 475694
/ allele="C"
/ allele="G"
/ db_xref="dbSNP:1052458"
gene complement(475811..479518)
/ gene="MGC2655"
/ note="Located on Accession NT_015360"
/ db_xref="LocusID:79228"
mRNA complement(join(475811..475982,476059..476193,
476279..476389,476486..476548,476643..476692,
476778..476880,476972..477043,477146..477194,
477271..477308,477393..477496,477571..477635,
477736..477847,479194..479366,479473..479518))
/ gene="MGC2655"
/ product="hypothetical protein MGC2655"
/ note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BLAST. Supporting evidence includes similarity to:
2 mRNAs"
/ transcript_id="NM_024339.1"
/ db_xref="GI:13236588"
/ db_xref="LocusID:79228"
CDS complement(join(475902..475982,476059..476193,
476279..476389,476486..476548,476643..476692,
476778..476880,476972..477043,477146..477194,
477271..477308,477393..477496,477571..477635,
477736..477818))
/ gene="MGC2655"
/ codon_start=1
/ product="hypothetical protein MGC2655"
/ protein_id="NP_077315.1"
/ db_xref="GI:13236589"

```

```

variation      /db_xref="LocusID:79228"
                476897
                /allele="A"
                /allele="G"
variation      /db_xref="dbSNP:960274"
                477561
                /allele="C"
                /allele="G"
variation      /db_xref="dbSNP:2245000"
                477859
                /allele="A"
                /allele="G"
variation      /db_xref="dbSNP:2717664"
                477927
                /allele="C"
                /allele="G"
gene           /db_xref="dbSNP:2526260"
                479612..480927
                /gene="FLJ20568"
                /note="Located on Accession NT_015360"
mRNA           /db_xref="LocusID:54985"
                join(479612..479712,480029..480085,480198..480326,
                480561..480927)
                /gene="FLJ20568"
                /product="hypothetical protein FLJ20568"
                /note="unclassified transcription discrepancy; Derived by
                automated computational analysis using gene prediction
                method: BLAST. Supporting evidence includes similarity to:
                1 mRNA"
                /transcript_id="NM_017885.1"
                /db_xref="GI:8923535"
                /db_xref="LocusID:54985"
CDS            join(479618..479712,480029..480085,480198..480326,
                480561..480696)
                /gene="FLJ20568"
                /codon_start=1
                /evidence=not_experimental
                /product="hypothetical protein FLJ20568"
                /protein_id="NP_060355.1"
                /db_xref="GI:8923536"
                /db_xref="LocusID:54985"
variation      480320
                /gene="FLJ20568"
                /allele="A"
                /allele="C"
variation      /db_xref="dbSNP:2285974"
                480781
                /gene="FLJ20568"
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:11042"
STS            480791..480911
                /gene="FLJ20568"
                /standard_name="RH41886"
                /db_xref="UniSTS:25755"
variation      480853
                /gene="FLJ20568"
                /allele="C"
                /allele="T"
                /db_xref="dbSNP:1050104"

```

```

gene      complement(481179..483199)
          /gene="FN14"
          /note="Located on Accession NT_015360"
          /db_xref="LocusID:51330"
          /db_xref="MIM:605914"
mRNA      complement(join(481179..481788,481870..482004,
          482240..482344,483067..483199))
          /gene="FN14"
          /product="type I transmembrane protein Fn14"
          /note="Derived by automated computational analysis using
          gene prediction method: BLAST. Supporting evidence
          includes similarity to: 3 mRNAs"
          /transcript_id="XM_036570.1"
          /db_xref="GI:14777984"
          /db_xref="LocusID:51330"
          /db_xref="MIM:605914"
STS       481211..481290
          /standard_name="STS-T56712"
          /db_xref="UniSTS:33040"
variation 481433
          /allele="T"
          /allele="C"
          /db_xref="dbSNP:1044326"
variation 481596
          /allele="A"
          /allele="G"
          /db_xref="dbSNP:13209"
CDS       complement(join(481733..481788,481870..482004,
          482240..482344,483067..483160))
          /gene="FN14"
          /note="Located on Accession NT_015360"
          /codon_start=1
          /protein_id="XP_036570.1"
          /db_xref="GI:14777985"
          /db_xref="LocusID:51330"
          /db_xref="MIM:605914"
variation 481739
          /allele="T"
          /allele="G"
          /db_xref="dbSNP:2232799"
variation 482140
          /allele="T"
          /allele="A"
          /db_xref="dbSNP:2232798"
variation 482262
          /allele="T"
          /allele="C"
          /db_xref="dbSNP:2232797"
variation 482438
          /allele="T"
          /allele="C"
          /db_xref="dbSNP:2232796"
variation 482558
          /allele="T"
          /allele="C"
          /db_xref="dbSNP:2232795"
variation 484040
          /allele="G"
          /allele="T"
          /db_xref="dbSNP:2526262"

```

```

variation      484161
                /allele="A"
                /allele="T"
                /db_xref="dbSNP:2526263"
variation      484199
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:2717704"
gene           485386..488845
                /gene="CLDN6"
                /note="Located on Accession NT_015360"
                /db_xref="LocusID:9074"
mRNA           join(485386..485410,487516..488845)
                /gene="CLDN6"
                /product="claudin 6"
                /note="Derived by automated computational analysis using
                gene prediction method: BLAST. Supporting evidence
                includes similarity to: 3 mRNAs"
                /transcript_id="XM_012518.3"
                /db_xref="GI:17487954"
                /db_xref="LocusID:9074"
variation      485972
                /gene="CLDN6"
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:2717703"
variation      487391
                /gene="CLDN6"
                /allele="G"
                /allele="C"
                /db_xref="dbSNP:2717701"
CDS            487537..488199
                /gene="CLDN6"
                /note="Located on Accession NT_015360"
                /codon_start=1
                /protein_id="XP_012518.1"
                /db_xref="GI:12739599"
                /db_xref="LocusID:9074"
variation      487963
                /gene="CLDN6"
                /allele="A"
                /allele="G"
                /db_xref="dbSNP:2257295"
variation      488861
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:2717700"
gene           complement(489542..490195)
                /gene="CLDN9"
                /note="Located on Accession NT_015360"
                /db_xref="LocusID:9080"
mRNA           complement(489542..490195)
                /gene="CLDN9"
                /product="claudin 9"
                /note="Derived by automated computational analysis using
                gene prediction method: BLAST. Supporting evidence
                includes similarity to: 1 mRNA"
                /transcript_id="NM_020982.1"
                /db_xref="GI:11141860"
                /db_xref="LocusID:9080"

```

CDS complement(489542..490195)
/gene="CLDN9"
/codon_start=1
/product="claudin 9"
/protein_id="NP_066192.1"
/db_xref="GI:11141861"
/db_xref="LocusID:9080"

variation 490295
/allele="G"
/allele="A"
/db_xref="dbSNP:2227269"

variation 490410
/allele="C"
/allele="A"
/db_xref="dbSNP:2231608"

variation 490414
/allele="C"
/allele="A"
/db_xref="dbSNP:2231607"

variation 490911
/allele="G"
/allele="A"
/db_xref="dbSNP:2231606"

variation 491006
/allele="T"
/allele="C"
/db_xref="dbSNP:2231605"

variation 491887
/allele="G"
/allele="A"
/db_xref="dbSNP:2717696"

variation 491956
/allele="A"
/allele="C"
/db_xref="dbSNP:2526264"

variation 492936
/allele="A"
/allele="T"
/db_xref="dbSNP:1548539"

variation 493019
/allele="A"
/allele="G"
/db_xref="dbSNP:2023913"

variation 494356
/allele="C"
/allele="T"
/db_xref="dbSNP:2526265"

variation 495678
/allele="C"
/allele="G"
/db_xref="dbSNP:2526267"

variation 495940
/allele="C"
/allele="G"
/db_xref="dbSNP:2526268"

STS 496210..496336
/standard_name="SHGC-60552"
/db_xref="UniSTS:74889"

STS 496216..496396
/standard_name="RH69739"

STS	/db_xref="UniSTS:81551" 496299..496429 /standard_name="SHGC-61135" /db_xref="UniSTS:56330"
variation	496999 /allele="C" /allele="T" /db_xref="dbSNP:2526270"
variation	497100 /allele="T" /allele="A" /db_xref="dbSNP:2717706"
variation	498102 /allele="C" /allele="G" /db_xref="dbSNP:2717674"
variation	498734 /allele="A" /allele="G" /db_xref="dbSNP:1635257"
variation	498736 /allele="A" /allele="G" /db_xref="dbSNP:1635258"
variation	498750 /allele="G" /allele="T" /db_xref="dbSNP:1635259"
variation	498754 /allele="A" /allele="G" /db_xref="dbSNP:1635260"
variation	498772 /allele="G" /allele="A" /db_xref="dbSNP:1236079"
variation	498800 /allele="T" /allele="C" /db_xref="dbSNP:1236078"
variation	498840 /allele="C" /allele="A" /db_xref="dbSNP:1236077"
variation	498852 /allele="G" /allele="C" /db_xref="dbSNP:1236076"
variation	498900 /allele="G" /allele="A" /db_xref="dbSNP:1236075"
variation	498908 /allele="C" /allele="A" /db_xref="dbSNP:1236074"
variation	498934 /allele="G" /allele="A" /db_xref="dbSNP:1236073"

```

variation      499010
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:1236072"
variation      499143
                /allele="A"
                /allele="G"
                /db_xref="dbSNP:2526271"
variation      499148
                /allele="T"
                /allele="G"
                /db_xref="dbSNP:1236071"
variation      499550
                /allele="G"
                /allele="C"
                /db_xref="dbSNP:2524316"
variation      499649
                /allele="A"
                /allele="C"
                /db_xref="dbSNP:2526272"
variation      500803
                /allele="C"
                /allele="G"
                /db_xref="dbSNP:986095"
variation      500983
                /allele="A"
                /allele="G"
                /db_xref="dbSNP:2526273"
gene           complement(501553..502260)
                /gene="LOC146440"
                /note="Located on Accession NT_015360"
                /db_xref="InterimID:146440"
mRNA           complement(join(501553..501999,502226..502260))
                /gene="LOC146440"
                /product="LOC146440"
                /note="Derived by automated computational analysis using
                gene prediction method: BLAST."
                /transcript_id="XM_085470.1"
                /db_xref="GI:18585774"
                /db_xref="InterimID:146440"
STS           501598..501680
                /standard_name="RH92900"
                /db_xref="UniSTS:85787"
CDS           complement(join(501712..501999,502226..502252))
                /gene="LOC146440"
                /note="Located on Accession NT_015360"
                /codon_start=1
                /protein_id="XP_085470.1"
                /db_xref="GI:18585775"
                /db_xref="InterimID:146440"
variation      502203
                /allele="C"
                /allele="T"
                /db_xref="dbSNP:2256045"
variation      502282
                /allele="A"
                /allele="C"
                /allele="G"
                /db_xref="dbSNP:1859377"
variation      502438

```



```

variation    /allele="A"
              /allele="G"
              /db_xref="dbSNP:1859378"
              502964
              /allele="A"
              /allele="G"
              /db_xref="dbSNP:2526274"
variation    503428
              /allele="G"
              /allele="C"
              /db_xref="dbSNP:2524315"
variation    504137
              /allele="T"
              /allele="G"
              /db_xref="dbSNP:984539"
variation    504189
              /allele="G"
              /allele="A"
              /db_xref="dbSNP:984538"
variation    505170
              /allele="A"
              /allele="G"
              /db_xref="dbSNP:2717692"
variation    509678
              /allele="G"
              /allele="C"
              /db_xref="dbSNP:2023874"
variation    515929
              /allele="C"
              /allele="T"
              /db_xref="dbSNP:739794"
variation    516721
              /allele="T"
              /allele="C"
              /db_xref="dbSNP:886429"
variation    516916
              /allele="T"
              /allele="C"
              /db_xref="dbSNP:886428"
variation    518275
              /allele="C"
              /allele="A"
              /db_xref="dbSNP:2005712"
variation    518782
              /allele="G"
              /allele="A"
              /db_xref="dbSNP:2335826"
gene          523712..530768
              /gene="PKMYT1"
              /note="synonym: MYT1; Located on Accession NT_015360"
              /db_xref="LocusID:9088"
              /db_xref="MIM:602474"
mRNA          join(523712..523913,526530..526897,527749..528242,
              528905..529011,529144..529316,529404..529561,
              530346..530423,530497..530768)
              /gene="PKMYT1"
              /product="membrane-associated tyrosine- and
              threonine-specific cdc2-inhibitory kinase"
              /note="unclassified transcription discrepancy; Derived by
              automated computational analysis using gene prediction

```

method: BLAST. Supporting evidence includes similarity to:
 1 mRNA
 /transcript_id="NM_004203.1"
 /db_xref="GI:4758927"
 /db_xref="LocusID:9088"
 /db_xref="MIM:602474"

CDS
 join(523904..523913,526530..526897,527749..528242,
 528905..529011,529144..529316,529404..529561,
 530346..530423,530497..530608)
 /gene="PKMYT1"
 /note="dual-specificity kinase phosphorylates Cdc2 on both
 Thr14 and Tyr15"
 /codon_start=1
 /product="membrane-associated tyrosine- and
 threonine-specific cdc2-inhibitory kinase"
 /protein_id="NP_004194.1"
 /db_xref="GI:4758928"
 /db_xref="LocusID:9088"
 /db_xref="MIM:602474"

variation
 529374
 /gene="PKMYT1"
 /allele="G"
 /allele="A"
 /db_xref="dbSNP:2074528"

variation
 529957
 /gene="PKMYT1"
 /allele="T"
 /allele="C"
 /db_xref="dbSNP:886427"

gene
 complement(530079..534194)
 /gene="LOC124222"
 /note="Located on Accession NT_015360"
 /db_xref="InterimID:124222"

mRNA
 complement(join(530079..532046,532183..532404,
 533721..534194))
 /gene="LOC124222"
 /product="similar to RIKEN cDNA 1500004C10"
 /note="Derived by automated computational analysis using
 gene prediction method: BLAST. Supporting evidence
 includes similarity to: 1 mRNA"
 /transcript_id="XM_058784.2"
 /db_xref="GI:18585776"
 /db_xref="InterimID:124222"

CDS
 complement(join(531613..532046,532183..532404,
 533721..533886))
 /gene="LOC124222"
 /note="Located on Accession NT_015360"
 /codon_start=1
 /protein_id="XP_058784.1"
 /db_xref="GI:17487953"
 /db_xref="InterimID:124222"

variation
 534927
 /allele="T"
 /allele="C"
 /db_xref="dbSNP:2285829"

gene
 complement(535182..539152)
 /gene="MGC10791"
 /note="Located on Accession NT_015360"
 /db_xref="LocusID:79412"

mRNA
 complement(join(535182..535751,536116..536245,

```

536322..536651,536766..536919,537112..537236,
537330..537421,538528..538702,538947..539152))
/gene="MGC10791"
/product="hypothetical protein MGC10791"
/note="Derived by automated computational analysis using
gene prediction method: BLAST. Supporting evidence
includes similarity to: 1 mRNA"
/transcript_id="XM_036566.1"
/db_xref="GI:14777965"
/db_xref="LocusID:79412"
variation 535980
           /allele="C"
           /allele="A"
           /db_xref="dbSNP:2285828"
CDS       complement(join(536223..536245,536322..536651,
536766..536919,537112..537236,537330..537421,
538528..538702,538947..539040))
           /gene="MGC10791"
           /note="Located on Accession NT_015360"
           /codon_start=1
           /protein_id="XP_036566.1"
           /db_xref="GI:14777966"
           /db_xref="LocusID:79412"
variation 536290
           /allele="C"
           /allele="A"
           /db_xref="dbSNP:2285827"
variation 540816
           /allele="G"
           /allele="A"
           /db_xref="dbSNP:757275"
variation 541178
           /allele="T"
           /allele="C"
           /db_xref="dbSNP:731722"
variation 541231
           /allele="T"
           /allele="A"
           /db_xref="dbSNP:731721"
variation 541253
           /allele="G"
           /allele="A"
           /db_xref="dbSNP:731720"
variation 542048
           /allele="G"
           /allele="C"
           /db_xref="dbSNP:986358"
variation 543123
           /allele="G"
           /allele="A"
           /db_xref="dbSNP:1544404"
variation 548706
           /allele="G"
           /allele="A"
           /db_xref="dbSNP:886430"
variation 548968..548969
           /allele="-"
           /allele="GA"
           /db_xref="dbSNP:3065589"
variation 548971

```

```

/allele="T"
/allele="C"
/db_xref="dbSNP:2335825"
variation 548973
/allele="G"
/allele="C"
/db_xref="dbSNP:2335824"
variation 551453
/allele="T"
/allele="C"
/db_xref="dbSNP:2057729"
STS 552394..552580
/standard_name="RH91964"
/db_xref="UniSTS:88733"
variation 552527
/allele="T"
/allele="C"
/db_xref="dbSNP:757277"
variation 552888
/allele="T"
/allele="C"
/db_xref="dbSNP:739796"
variation 553036
/allele="T"
/allele="C"
/db_xref="dbSNP:739795"
gene complement(553752..570411)
/gene="DKFZp761A132"
/note="Located on Accession NT_015360"
/db_xref="LocusID:84256"
mRNA complement(join(553752..554873,563469..563529,
565105..565377,566177..566439,567135..567228,
568893..568945,569581..569844,569978..570411))
/gene="DKFZp761A132"
/product="hypothetical protein DKFZp761A132"
/note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BLAST. Supporting evidence includes similarity to:
1 mRNA"
/transcript_id="NM_032296.1"
/db_xref="GI:14150048"
/db_xref="LocusID:84256"
STS 553766..553867
/standard_name="SHGC-60766"
/db_xref="UniSTS:81466"
variation 554264
/allele="G"
/allele="A"
/db_xref="dbSNP:757276"
variation 554344
/allele="G"
/allele="A"
/db_xref="dbSNP:734138"
CDS complement(join(554834..554873,563469..563529,
565105..565377,566177..566439,567135..567228,
568893..568945,569581..569844,569978..570251))
/gene="DKFZp761A132"
/note="putative protein; unclassified translation
discrepancy"
/codon_start=1

```

```
/evidence=not_experimental
/product="hypothetical protein DKFZp761A132"
/protein_id="NP_115672.1"
/db_xref="GI:14150049"
/db_xref="LocusID:84256"
variation 562208
           /allele="A"
           /allele="C"
           /db_xref="dbSNP:1029442"
variation 563657
           /allele="A"
           /allele="C"
           /db_xref="dbSNP:1060484"
variation 563678
           /allele="A"
           /allele="G"
           /db_xref="dbSNP:1060485"
variation 566235
           /allele="G"
           /allele="C"
           /db_xref="dbSNP:1007477"
variation 566559
           /allele="A"
           /allele="G"
           /db_xref="dbSNP:2074357"
variation 566721
           /allele="C"
           /allele="G"
           /db_xref="dbSNP:2074358"
variation 567130
           /allele="A"
           /allele="G"
           /db_xref="dbSNP:739716"
variation 568693
           /allele="A"
           /allele="G"
           /db_xref="dbSNP:2074359"
variation 569065
           /allele="A"
           /allele="G"
           /db_xref="dbSNP:2074360"
variation 569113
           /allele="A"
           /allele="G"
           /db_xref="dbSNP:2074361"
variation 570078
           /allele="C"
           /allele="G"
           /db_xref="dbSNP:2074362"
variation 570423
           /allele="A"
           /allele="G"
           /db_xref="dbSNP:2074363"
variation 570680
           /allele="C"
           /allele="T"
           /db_xref="dbSNP:2074364"
variation 581076
           /allele="A"
           /allele="C"
```

variation	/db_xref="dbSNP:1981538" 581307..581308 /allele="-" /allele="CA"
variation	/db_xref="dbSNP:3066612" 581528 /allele="T" /allele="G"
variation	/db_xref="dbSNP:2335858" 582878 /allele="A" /allele="G"
variation	/db_xref="dbSNP:1966334" 582938 /allele="C" /allele="T"
variation	/db_xref="dbSNP:1966335" 582939 /allele="A" /allele="G"
variation	/db_xref="dbSNP:1966336" 582941 /allele="C" /allele="T"
variation	/db_xref="dbSNP:1966337" 583059 /allele="G" /allele="T"
variation	/db_xref="dbSNP:1468214" 588265 /allele="T" /allele="G"
variation	/db_xref="dbSNP:2335544" 589277 /allele="C" /allele="T"
variation	/db_xref="dbSNP:2074365" 589470 /allele="A" /allele="G"
variation	/db_xref="dbSNP:886322" 589750 /allele="C" /allele="T"
variation	/db_xref="dbSNP:886323" 590032 /allele="A" /allele="G"
variation	/db_xref="dbSNP:757164" 590243 /allele="C" /allele="T"
variation	/db_xref="dbSNP:757165" 590299 /allele="C" /allele="G"
variation	/db_xref="dbSNP:757166" 597791 /allele="G" /allele="C"

```

variation      /db_xref="dbSNP:1468261"
                600388
                /allele="G"
                /allele="A"
variation      /db_xref="dbSNP:2335542"
                600473..600474
                /allele="-"
                /allele="CA"
variation      /db_xref="dbSNP:3033174"
                602505
                /allele="G"
                /allele="C"
gene           /db_xref="dbSNP:1859255"
                complement(604177..620345)
                /gene="LOC114984"
                /note="Located on Accession NT_015360"
mRNA           /db_xref="InterimID:114984"
                complement(join(604177..604510,606788..607207,
                608239..608339,620193..620345))
                /gene="LOC114984"
                /product="similar to putative"
                /note="Derived by automated computational analysis using
                gene prediction method: BLAST. Supporting evidence
                includes similarity to: 1 mRNA"
                /transcript_id="XM_054962.3"
                /db_xref="GI:18585777"
                /db_xref="InterimID:114984"
variation      604208
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:2301764"
variation      604312
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:1052168"
variation      604351
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:1052167"
CDS            complement(join(604410..604510,606788..607109))
                /gene="LOC114984"
                /note="Located on Accession NT_015360"
                /codon_start=1
                /protein_id="XP_054962.1"
                /db_xref="GI:16165279"
                /db_xref="InterimID:114984"
variation      606214
                /allele="T"
                /allele="G"
                /db_xref="dbSNP:1859254"
variation      606546
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:2285826"
variation      606597
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:2285825"
variation      607127
                /allele="G"

```

	/allele="A"
variation	/db_xref="dbSNP:2285824"
	608312
	/allele="G"
	/allele="C"
variation	/db_xref="dbSNP:1063677"
	608470
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:2301763"
	612166
	/allele="T"
	/allele="C"
variation	/db_xref="dbSNP:2015260"
	612240
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:1034709"
	612701
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:2335465"
	613410
	/allele="T"
	/allele="G"
variation	/db_xref="dbSNP:2878435"
	615319
	/allele="C"
	/allele="A"
variation	/db_xref="dbSNP:2335464"
	619243
	/allele="G"
	/allele="A"
variation	/db_xref="dbSNP:2335462"
	619386
	/allele="T"
	/allele="A"
variation	/db_xref="dbSNP:2335461"
	620280
	/allele="G"
	/allele="C"
variation	/db_xref="dbSNP:1063676"
	620523
	/allele="T"
	/allele="A"
	/db_xref="dbSNP:2285823"

Mail Stop Amendment KAM/sid

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Date: December 20, 2005
Doc. No. 5470-368
Serial No. 16/511 989
Inventor: Ting et al

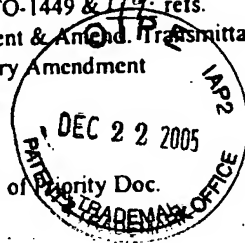
Sir: Kindly acknowledge receipt of the accompanying items listed below
by placing your receiving stamp hereon and return mailing:

Application Transmittal and:

- ☐ Specification pages
- ☐ No. of Claims
- ☐ Declaration & POA
- ☐ Assignment and Fee
- ☐ Small Entity Statement
- ☐ Formal Drawings/ sheets
- ☐ Associate Power of Attorney
- ☐ Exp. Mail ☒ 1st Class Mail

☒ Other: return postcard

- ☐ Check \$
- ☒ IDS & PTO-1449 & 119 refs.
- ☐ Amendment & Amend. Transmittal
- ☐ Preliminary Amendment
- ☐ Issue Fee
- ☐ Brief
- ☐ Appeal
- ☐ Submittal of Priority Doc.



Respectfully submitted,
MYERS BIGEL SIBLEY & SAJOVEC, P.A.
Attorneys for Applicant